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JOURNAL MEDLINE COMMENT	TITLE	AUTHORS	השממשמט ב	ORGANISM	KEYWORDS	VERSION	ACCESSION	LOCUS	STACNA
J. Biol. Chem. 267 (7), 4766-4772 (1992) 92165839 On Aug 30, 1993 this sequence version replaced g1:386712.	Lindberg, M. and Hook, M.  Molecular characterization and expression of a gene encoding a Staphylococcus aureus collagen adhesin [published erratum appears in 7 Biol Chem 1994 Apr 15: 269/15):116721	Patti, J.M., Jonsson, H., Guss, B., Switalski, L.M., Wiberg, K.,	Bacteria; Firmioutes; Bacillus/Clostriaium group; Bacillus/Staphylococcus group; Staphylococcus.  1	Staphylococcus aureus Staphylococcus aureus	cna gene; collagen adhesin.	M81736.1 GI:387879	Scapnylococcus aureus collagen adnesin (cha) gene, complete cus. M81736	STACNA 3827 bp DNA BCT 17-AUG-1994	

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GQQVKYTVEELTKVGYTTHVDNNDMGHLIVTNKYT PETTSISGKVWDDKDNODGKR
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PEKYSYNLLADGEKVKTJUTYSETNMKY EFKDLPKYDBGKKIBYTYTEDHYKDYTDI
NGTTITNKYTPGETSATYTKNWDDNNNQDGKRPTEIKVELYQDGKATGKTAILNESNN
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EDTTPEGYTKKENGLVVTNTEKPIETTSISGEKVWDDKDNQDGKRPEKVSVNLLANGE
KVKTLDVTSETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDINGTTITNKYTPGE
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/transl_table=11
/product="collagen
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137. .3702
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/db_xref="taxon:1280"
/tissue_lib="FDA 574; lambda gtl1"
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/protein_id="AAA20874.1"
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Switalski,L.
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Collagen binding protein as well as
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Patent: US 5831794-A 1 22-DEC-1998;
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synthetic construct
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A18434
A18434.1 GI:513301
                                                                                                                                Patent:
                                                                                                                                                                        artificial sequence.
1 (bases 1 to 3468)
                                                                                                                 COLLAGEN BINDING PROTEIN AS WELL atent: WO 9207002-A 1 30-APR-1992; Location/Qualifiers
                                                                                                                                                                                                                                                                           DNA molecule comprising a nucleotide sequence from S for a protein or polypeptide having collagen binding
                                                                                                                                                                                                                                                                                                                                                                                                    849
                                          translation"
                                                                     /db_xref="taxon:32630"
1. 3465
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                                                                                                                                                                                                              construct.
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keevngksfnhthninaagestrikologgoldjethinturgokefvnnsqawqoeh
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gttkvtmokldnoggkrerekvaldkologkreteltkvkgdtholtsetnukverlddysethelt
sissekvaddkologokrekvaldkologokretikvkgytthungek
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gokreteltveldokkriettissekvaddkologokretikvkgthladsekvkthdbund
gokreteltveldokkriettissekvaddkologokretekregvynllangek
vktldvtsetnukvetetsolpkkrdskatsgovynttelekregetkv
kktyttramdnungdgkreteirveldygkatsgratinesumpthtytiktest
sapvtramdletskek
govkytteltvnkytpetikveltygokatsgratinesumpthtytgetekpd
sapvtramen
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REFERENCE
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TITLE
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1 GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAAGTGGCATGGCCGACAAGC 60
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A18436.1 GI:513303
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Location/Qualifiers
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                                      Conservative
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LDLGTLNINVTGTHSNYYSGQSAITDDEKAFPGSKITYDNIKWTIDVTIPQGYGSYNS
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CEXYMDDAGNLOKAGAGATOKTAT
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676 c 868 g 1122 t
                                                                                                                                                                                          GKATGKTAILNESNNWTHTWTGLDEKAKGQQVKYTVDELTKVNGYTTHVDNNDMGNLI
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                                                                                                                                                                                                                                                       GEKVWDDKDNQDGKRPEKVSVNLLANGEKVKTLDVTSETNWKYEFKDLPKYDEGKKIE
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                                                                                                                                                                                                                                 YTVTEDHVKDYTTDINGTTITNKYTPGETSATVTKNWDDNNNQDGKRPTEIKVELYQD
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                                    Score 792.2; DB 6;
Pred. No. 5.1e-127;
0; Mismatches 13;
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                                      Indels
                                                                      Length 4612;
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December   December	KEYWORD SOURCE ORGAN REFEREN AUTHO	RESUI ARO67 LOCUS DEFIN ACCES	Db	Qy	Оy	D .	Q V	Dy Dy	Db	γQ	Дy	Ωу	Qy	Qу Db	Qу	ОУ	ОУ	Qу Db	Qy Db	Db
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	Unknown. Unknown. Unclassified. 1 (bases 1 to 4612) 1 (bases, Hook, M., Jonsson, H., Lindberg, M., Patti, J., Signas, C. an	AR067712 4612 bp DNA PAT 29-SEP-199 Sequence 8 from patent US 5851794. AR067712 AR067712.1 GI:5998934	ATAAAGATACCAAG 196	ATAAAGATACCAAG 84	TTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAG 834 		атсаассатсствассаассаастсаассасаастсатттватсатастстссасаст 77 <i>4</i>	ACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGG 714 	ACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC 177	ACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC 65	CAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG 59 	TAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT 534 	TPATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGAT 474 	ATGCTACC-AGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAA 414 	CGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAG 355 	AAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 300 	AATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAATTTAACGCAA 240 	TGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180 	GTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG 120 	117

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                                                                                                 TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAAT
                                                                                                                                                TACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGG
                                                                                                                                                                                  AACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC
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                                              ATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAG
                                                                                   TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAAT
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US 5851794-A 8 22-DEC-1998;
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679 c 864 g
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CAAAGTGCAATTACTGAATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAAT 588
                                                       GAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAG
                                                                                                                                                                                                      TCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAA 348
                                                                                                                                                                                                                                                                                                                                                      AATTTAACGCAAACAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAA 288
                                                                              TTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGA 528
                                                                                                                                                                                                                                           ACGGGAGATATGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 El-Sayed,N.M., Ghedin,E., Song,J., Larkin,C., Wanless,D., Jones,K Peterson,J., Hou,L., Zhao,H., Mason,T., Milischer,J., Pai,G., Van Aken,S., Utterback,T., Khalak,H.G., Gerard,C., Leech,V., Ullu,E., Melville,S., White,O., Adams,M.D., Donelson,J.E. and Fraser,C.M., Trypanosoma brucei GUTatlO.1 RPC193-3H15 BAC genomic sequence
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Trypanosoma brucei chromosome II o
IN PROGRESS ***, 1 ordered pieces
AC007926
AC007926.8 GI:14787210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medical Center Dr, Rockville, MD 20850, USA
On Jul 17, 2001 this sequence version replaced gi:12746529.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              El-Sayed, N.M., Khalak, H. Direct Submission
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is believed to be correct as given, however the of the gaps between them are based on estimates provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is availa the accession number will be preserved.

1 155204: contig of 155204 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-007-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
On Dec 11, 2000 this sequence version replaced gi:11230847.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced

* this sequence will be replaced
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1 (bases 1 to 171798)

1 (bases 1 to 171798)

El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K. El-Sayed, N.M., Ghedin, E., Shao, H., Mason, T., Milltscher, J., Pai, G., Van Peterson, J., Hou, L., Zhao, H.G., Gerard, C., Leech, V., Ullu, E., Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Aken, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTattl0.1 RPC193-1118 BAC genomic sequence
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Trypanosoma
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Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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171798: contig of 171798 bp in length.
Location/Qualifiers
1. .171798
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                                                                                       Conservative
                                                                                                                                                                                                                        /chromosome="unknown"
/clone="RPCI93-1I18"
37575 c 33263 g 6
                                                                                                                                                                                                                                                                                                               /organism="Trypanosoma
/isolate="GUTat10.1"
                                                                                                                                                                                                                                                                                           /db_xref="taxon:5691"
                                                                                                         7.7%;
                                                                                                         Score 65.6; DB 2; Pred. No. 0.016;
                                                                                     Mismatches
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                                                                                                                                                                                                                                        101 TAACTGTTAAAGGTGAACAGGTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTA 160
                                                                                                                                AAGGAAGAATTTAACGCAAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTG
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                                                  GGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCT 340
                                                                                                       TTAAAAGTTTTAAAACAGGA 836
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166494
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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577 ACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATAT 636
                                                                                                                                                                                                               AATATTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAA 456
                                                                       TATTATAGTGGAÇAAAGTGCAATTACTGATTTTTGAAAAAAGCCTTTCCCAGGTTCTAAAAATA 576
                                                                                                               GGTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAAT 516
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                                                                                                                                                                                                                                                                  209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-70V-1999) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA On Jul 17, 2001 this sequence version replaced gi:12746529.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the sizes for the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., V Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E. Melville, S., White, O., Adams, M.D., Donelson, J. E. and Fraser, C.M. Trypanosoma brucei GUTatl0.1 RPCI93-3H15 BAC genomic sequence
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Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        El-Sayed, N.M., Khalak, H. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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1 (bases 1 to 155204)
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1 155204: contig of 155204 bp in length.
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31603 c 32329 g
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/chromosome="II"
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* NOTE: This record contains 253 individual

* NOTE: This record contains 253 individual

* contigs. Runs of Nare used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-OCT-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 208546) Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens clone
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Mammalia; Eutheria; Primates;
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Naliapareddy, S.R., Singh, K.V., Duh, R.W., Weinstock, G.Murray, B.E.
Diversity of ace, a gene encoding a microbial surface
                                                                                                                                                                                                           AF260878 1822 bp DNA BCT 18-OCT-2. Enterococcus faecalis strain LBJ-1/TX0020 collagen adhesin
                                                                                    Enterococcus faecalis Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                              precursor (ace) gene, complete cds AF260878
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                                     Singh, K.V., Duh, R.W., Weinstock, G.M. and
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                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                      1 GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAGTGGCATGGCCGACAAGC
                                     ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 300
                                                                                                        AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAAGTTTAACGCAA 240
                                                                                                                                                                                                               GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180
CCGAATGTGATAGAAACGGATTTCGGAACAGCAACGGCGACTCAACGTTTGACGATTGAA
                                                                                  CATAATGTGAATGGGCATTTTTCTTTCGGGATTAAAACGCTTATCACCAATAGTTCGCAA
                                                                                                                                                                       GAAGTTTTTATCTATAAAGATCATGTTGTAGCAACATTTAACGAAAAAGTTGAATCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recognizing adhesive matrix molecules, from different strains of enterococcus faecalis and evidence for production of ace during
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/note="Region: /
1107. .1787
/gene="ace"
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TESSLDIPLETI EEWEPKTPTSEGATETSEKTDTTETVESSOPEVVSSTEESBNPDES
ETLGTISPI I PEKPSVTTEENGVTETAESSOPEVHVSPTEEBENLDESETLGTISPI PE
EKPSVTTEENGATETAESSQPEVHVSPTKEITTEKKOPSTETTVETNKTITSKNOPQ
ILNAPLNTLKNEGSPOLAPGLLSEPIQKLNEANGGRELPKTGTTKTPFMLIAGILAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="collagen adhesin precursor"
/protein_id="AAG23936.1"
/protein_id="AAG23936.1"
/db_xref="Gi:10863216"
/translation="MTKSVKFLVLLLVMILPIAGALLIGPISFGAELSKSPIVDKVEL
DHTTLYOGEMTSIKVSFSDKENOKIRPGDTITLTLEGALVGMTENDGSPRKINLNGLG
EVFIYKDHVVATFNEKVESVHNVNGHFSFGKIKTLITNSSQPNVIETDGTATATATGTE
IEGVTNTETGOIERDYPFFYKVDLLAGESNQVEMFLNVELNKSDVTEDISIADEGGSG
QQLNKESFTFDIVNDKETKYISLAEFEQQGYGKIDFVTDNDFNLRFYRDKARFTSFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ace"
141. .1109
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328 c 359
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/strain="LBJ-1/TX0020"
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518 ATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAAGCCTTTCCAGGTTCTAAAATAA 577
                                                                                                                                                                            398 ATATTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAG 457
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                                                                                   GTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATT 517
                                                                                                                                  TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGAC 529
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                                         GGCGATTTGGCTGGAGAGTCAAATCAAGTACGTTGGTTTTTAAATGTGAACCTCAATAAA
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On Aug 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on Aug 24, 1999 this sequence version replaced g1:5731882. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.IMPORTANT: The sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phage etc.
Order of segments is not known; 800 n's separate segments
NOTE: This is a 'working draft' sequence.
NOTE: This is a 'working draft' sequence.
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Plasmodium falciparum chromosome 13 strain
PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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/chromosome="13"
29264 c 27321 g 11:
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/strain="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005504 104992 bp DNA
Plasmodium falciparum chromosome
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Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria parasite P. falciparum Plasmodium falciparum
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                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                  Apr 2, 1999 this sequence version replaced gi:4337172. NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 104992)
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                  /organism="Plasmodium
/db_xref="taxon:5833"
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91011: contig of 32169 bp in length
91211: gap of unknown length
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Matches

Conservative

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Gaps

7.2%; 43.6%;

Score 61.4; DB Pred. No. 0.088; Mismatches

Length 104992; Indels

Best Local Similarity

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JOURNAL
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                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; 1 (bases 1 to 169546)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                              HTG; HTGS_PHASE1.
malaria parasite P. falciparum
                                                                                                                                                                                                                                              Plasmodium falciparum chromosome 12 clone PROGRESS ***, 2 unordered pieces.
Direct Submission Stanford DNA Sequencing Submitted (19-FEB-1998) Stanford DNA Sequencing
                                                                                                                                                                Plasmodium falciparum
                         Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W
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                               GATGTA---ACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACAAA 660
                                                                                                                                                                                                                                                                                       TCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAAGATTTAAGCACA 483
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                                                                                                                                                                        AAAAATAACATTGAAAAAATGATAATAATCATAATAGCAAAAATAATGAATATAATGAG
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  AATGTATATAATAGTGATAAAATATCTTTTCAAAATCAACCTGAAATAATTTACTCAAAT 75595
                                                                                                                             GATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACACAATT 603
                                                                                                                                                                                                            TTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATTACT
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                                                                                                                                                                                                                                                                                                                                                  TCAGATGATGTCAAAATATTTAATGAGAATTCAAATAATGAAAATAAGAAAAAGGTGAAA 7535
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94304, USA
On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* is not known and their order in this sequence record is
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RESULT 15
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WPCOMMENT
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Fragment Name Begin End PFMAL4P1 1 11000

PFMAL4P1_0 1 10001

PFMAL4P1_1 100001 210000

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PFMAL4P1_3 300001 392633

Continuation (2 of 4) of PFMAL4P1 from base 100001 (AL034557 Plasmodium falciparum chrom
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Best Local Similarity 44.0%;
31725 AGGAAGATTTTATTGATTTTAAAGAAAATAT 31755
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                                                                                                   704 CACAAGCTTGGTATCAAGAGCATGGTAAGGAAGGTGAACGGGAAATCATTTAATCATA 763
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                                   CTGTGCACAATATTAATGCTAATGCCGGTAT 794
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                                                                        AATATAATGTTGATGATTATCATGAGGTGCAGGATGGTCAGGACGAATCATTTAAAGAAG 3172
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Search completed: January 29, 2002, 23:20:55 Job time: 6639 sec

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Maximum DB
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	AL057309 Drosophil		AL063632 Drosophil	N		AL514901 AL514901								-	ğ	AL441457 T7 end of	ผั	••		AL436389 T7 end of	B12681 F27D1-Sp6.1		AL226115 Tetraodon							AL060767 Drosophil		AL061917 Drosophil

## ALIGNMENTS

REFERENCE AUTHORS TITLE MEDLINE REFERENCE REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT CNS06X9S SOURCE DEFINITION JOURNAL MEDLINE TITLE ORGANISM TITLE JOURNAL AUTHORS JOURNAL 2 (bases 1 to 1007)
2 (bases 1 to 1007)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000) CNSU6X9S 1007 bp DNA GSS 06-JUL-2001 T3 end of clone AXOAA039F08 of library AXOAA from strain CBS 7064 of Pichia farinosa, genomic survey sequence. Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux; CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: 1 (bases 1 to 1007)
de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Potier, S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia Pichia farinosa. Pichia farinosa FEBS Lett. 487 (1), 87-90 (2000) 20584725 AL419462.1 GSS. Genoscope sorbitophila Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia. (bases 1 to 1007) GI:12202640

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                     DEFINITION
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Best Local Similarity 36.9%;
Matches 217; Conservative 6
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                                                                                                                                                                                                                                                               WAWAAAAAAAAAAAAAAWWTAAAWAAATGAAATAAAAGATTAAWWAWAAAAAWAWA
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                                                                                                                        AACGTTTAGTGGGGGAATAAAAAAACTAAAATTAAAAATAATATCAAG
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Drosophila melanogaster genome survey sequence BACR29B23 of RPCI-98 library from Drosophila me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                   CNS00EVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 kb were prepared and both extremities were sequenced. keywords for description of this sequence and for the sether extremity of this insert.
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/strain="CBS 7064"
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/clone="AxOAAO39F08"
/clone_lib="AXOAA"
/note="end: T3"
a 86 c 126 g 161 t
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Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                                                                                                                484 TTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATTACT
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TTWAAATAWAAAAAAAAAAAAAAWATWAAWAATWATAWATAAWTTAAAAWAATAAAAWA
                                                                                                                                                                                                                                                                                                                                                                                                                        ATACGACACATGTACGA-----TGGTTTTTAAATATTAACAATGAAAAAAGTTATGTA 423
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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/clone="BACR29B23"
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a 91 c 60 g
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.9%; Score 67.4; DB 13; 32.2%; Pred. No. 0.0017; ative 110; Mismatches 288;
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                                                                                                                                       Query Match
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                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ946120 641 bp DNA GSS Sheared DNA-46J23.TR Sheared DNA Trypanosoma Sheared DNA-46J23, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
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Other_GSSs: Sheared DNA-46J23.TF
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Gerrard, C., Leech, V., de
Fraser, C. and Adams, M.
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1 (bases 1 to 641)
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                                                                       Conservative
                                                                                                                                                                                                                                                                                            /clone_"Sheared DNA-46J23"
/clone_lib="Sheared DNA'
/clone_lib="Sheared DNA'
/clone_"Vector: pUC18; Site_l: Smal; Constructed at The
/note="Vector: pUC18; Site_l: Smal; Construction of Construct
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/strain="TREU927/4 GUTat
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de Jong,P., Ullu,E., Melville,S., Donelson,J.
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hes 320;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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    Web : www.genoscope.cns.fr)

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   Submitted (23-JUL-1999)
BP 191 91006 EVRY cedex
                                                                                 Plasmid Drosophila melanogaster
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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        AATDTDAKRAAAGRRKRDARKTARDGGRRARTRRRAWAAGGKRARAGARRARAADD

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         fruit fly.

Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                              Drosophila melanogaster genome survey sequence BACN01115 of DrosBAC library from Drosophila me
                                                                                                        GSS
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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/note="end : SP6"
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/plasmid="pBeloBAC11"
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                                  ATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACAAAAACCA 664
                                                                                                                                                TAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATTACTG
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ATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACACAATTG
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BAN01115"
/note="end : T7"
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                            AACATCTGGGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAG
                                                               AAAAGAAAAAAAAGTWAATAAAAAAAAAATATGTGAAAKAWAAAAATATAGTAWAA
                                                                                                                              ATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAGGATAAAGATA 844
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                                                                                                                                                                                             271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Anopheles gambiae GSS T7 end of clone 14D07 of NotreDamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-2000) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr) 2 (bases 1 to 879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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licoidea; Anopheles.
(bases 1 to 879)
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/note="end:: T7"
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/clone="14D07"
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/strain="PEST"
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TITLE
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                                                                                                                                             Submitted (23-JUI-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                     Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
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 /organism="Drosophila m
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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                                   TATAATAGTTTTTCAATTAACTACAAAACCAAAATTACGAATGAACAGCAAAAAGA 689
                                                                                                                   ATAACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGGTCA
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TAAWTWTAWTTAATWTAAWAATAAAWATAAAAATWAWAAWWAWATAAWWTAAAAA 993
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN10102 of DrosBAC library from Drosophila melanogaster (fruit
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High quality sequence stop: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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T24D11-Sp6 TAMU Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                Tel: 215-898-9384
Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Ecker J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                jecker@atgenome.bio.upenn
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                                                                                                                                                  /note="Vector: BeloBACII; Site_1: HindIII;
; Produced by Rod Wing"
50 c 53 g 678 t 372 others
                                                                                                                                                                                                /sex="hermaphrodite"
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Plasmid Drosophila melanogaster
Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota;
Pterygota; Prosophila.
             - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome sur BACN15Al2 of DrosBAC library from
                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequenca
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns
                                                                                                                                                                                                    Direct Submission
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BP 191 91000 6000 CORS.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila The BDGP is constructing a physical map of the Drosophila
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                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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  AATTAAAAATTGAAAAAA
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                                                                                                                               ACTGTGCACAATATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAAGGTGAATTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
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                                                                                                               GGTGGACAGCAGTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAAT 516
                                                                                                                                                                                                                            190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C. Gerrard,C., Leech,Y., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Addms,M.

Determination of clone end sequences from Trypanosoma brucei GUTat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
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Other_GSSs: Sheared DNA-42E21.TR
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de Jong, P., Ullu, E., Melville, S., Donelson, J.
                                                                                                                                                                                                                                                                                                    Score 59.2; DB 13; Pred. No. 0.065;
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                                                                    GGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAAAAA 183
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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RESULT 2  A48620  Adhesin - Staphylococcus aureus (fragment) C:Species: Staphylococcus aureus C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 C:Accession: A48620 R:Patti, J.M.; Boles, J.O.; Hook, M. Biochemistry 32, 11428-11435, 1993 A;Title: Identification and biochemical characteriz A;Reference number: A48620; MUID:94032261 A;Accession: A48620	Qy 12 SDDKVATITSGNKSTNVTVHKSEAGTSSVFYY-KTGDM-LPEDTTHVRWFLNINNEKSYV [	RESULT 1  A42404  collagen adhesin - Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Chate: 04-Mar-1993 #sequence_revision 18-Nov-199. C;Accession: A42404; S27665 R;Patti, J.M.; Jonsson, H.; Guss, B.; Switalski, I J. Biol. Chem. 267, 4766-4772, 1992 A;Title: Molecular characterization and expression A;Reference number: A42404; MUID:92165839 A;Contents: FDA 574 A;Accession: A42404 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1185 <pat> A;Cross-references: EMBL:M81736 A;Note: sequence extracted from NCBI backbone (NCI) A;Note: sequence extracted from NCBI backbone (NCI) Best Local Similarity 90.1%; Pred. No. 4.3e-1 Matches 182; Conservative 2; Mismatches</pat>	ALIGNMENTS	30 90.5 8.1 784 2 JH0101 31 90 8.0 669 2 S14535 32 90 8.0 858 1 A42239 33 90 8.0 4688 2 F82885 34 89.5 8.0 454 2 T26296 36 89.5 8.0 496 2 S61327 37 89.5 8.0 1584 2 T262674 38 89.5 8.0 1584 2 T262674 39 89.5 8.0 1258 2 C81169 39 89.5 8.0 2893 2 A64556 40 89 7.9 599 2 S61318 41 89 7.9 590 2 T46261 42 89 7.9 1166 2 T28680 44 89 7.9 1166 2 T28680 45 89 7.9 11553 2 T18502
94 #text_change 03-Mar-1995 rization of the ligand binding domain	1-LPEDTTHYRWFLNINNEKSYV 69	1994 #text_change 10-Nov-1995 i, L.M.; Wiberg, K.; Lindberg, M.; Hook sion of a gene encoding a Staphylococcu (NCBIP:83982) DB 2; Length 1185; 3e-58; 16; Indels 2; Gaps 2;		apolipoprotein B-1 asparagine-rich pr adenylate cyclase hypothetical prote transcription fact hypothetical prote IgA-specific metal hypothetical prote IgA-specific metal hypothetical prote IgA-specific metal coxin-like outer m hypothetical prote laccase (EC 1.10.3 conserved hypothet fibrinogen-binding glucosyltransferas hypothetical prote

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R;Status: preliminary

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A;Title: The complete genome sequence of the lactic acid bacterium.
A;Reference number: A86625
A;Accession: D86710
                              A; Experimental C; Genetics:
                                                         A;Cross-references: GB:AE005176; NID:g12723592; PIDN:AAK04782.1; GSPDB:GN00146 A;Experimental source: strain IL1403
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A;Note: sequence extracted from NCBI backbone (NCBIP:138726)
A;Gene: icaC
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26.5%;
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Pred. No.
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3.8e-08;
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A43855
R;Barenkamp, S.J.; Leininger, E.
Infect. Immun. 60, 1302-1313, 1992
Infect. Immun. 60, 1302-1313, 1992
Infect. Immun. 60, 1302-1313, and DNA sequence analysis of genes encoding results and sequence analysis of genes encoding results.
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis
c;Spectes: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81888
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1536 <BAR>
A;Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)
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                                                                                                                                                                                        KEEVNGKSFNHTVHNINANAGI
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Pred. No. 26;
33; Mismatches
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Pred. No. 0.16;
28; Mismatches
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R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Nature 404, 502-506, 2000

A; Title: Complete DNA sequence of a A; Reference number: A81775; MUID:203

MUID:20222556

serogroup A strain of Neisseria

menigitidis

22491

S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;

S.R.; Mo Rajandre

Mungall,

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A:Status. r--
A:Mocule type: DNA
A:Residues: 1-4919 <WAR>
A:Residues: EMBL:AF057696;
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C;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 *sequence_revision 22-Oct-1999 *text_change 22-Oct-1999
C;Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like prote
A;Reference number: Z20984; MUID:99030326
A;Accession: T31105
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-592 < PAR>
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Matches 43
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                                                                                                                                                                                                     75 IKDQIQGGQQLDLST-----LNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  1spA2
                                      EVNGKSFNHTVHNINANAGIEGTVKGE-LKVLKQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSDDKVATITSGNKSTN------VTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWF 59
                                                                               TKNFKSIGDLINEALSDSAPEAIEAYYSGSSSNYINPVSYLAALGNANNSS:
                                                                                                                      TKN-----TIDVTIPQGYGSYNS-FSINYKTKITNEQQKEFVNNSQAWYQEHGKE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNHTVHNINANAGIEGTVK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGK-----GKGE-NGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGST-----LTDTLAGSSASHV--- 198
-- NPHYLNTALKHILGNGWQDDLKKQENIKVLKQ 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DAGNOSTHYTRAASIKDVLNAGW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                             h 8.8%; Score 98.5; DB 2;
Similarity 24.8%; Pred. No. 1.4e+02;
53; Conservative 34; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g3929021; PID:g3929023; PIDN:AAC79761.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIKGVKTGSTTGQSENVDFVRTYDTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
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RESULT S33851

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69

VSK-DITIKDQIQGGQQLDL----STLNINVTGTH---

-SNYYS 103

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                                          Q
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                                                                                                                                                                                                                                                                                                                                                           A; Authors: Smith, H.O.; Venter, J.C. A; Title: Genomic sequence of a Lyme disease A; Reference number: A70100; MUID:98065943 A; Accession: C70203
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA topoisomerase I (topA) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: fnbB
A;Start codon: TTG
C;Keywords: fibronectin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1117 <LIN>
A;Residues: 1-1117 <LIN>
A;Cross-references: EMBL:Z22151; NID:g288970; PIDN:CAA80122.1; PID:g581643
A;Note: the authors translated the initiation codon TTG for residue 1 as L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Lindgren, P.E.; McGavin, M.J.; Signaes, C.; Guss, B.; Guru
Eur. J. Biochem. 214, 819-827, 1993
A;Title: Two different genes coding for fibronectin-binding
A;Reference number: S33850; MUID:93307299
A;Accession: S33851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibronectin-binding protein precursor - Streptococcus dysgalactiae C;Species: Streptococcus dysgalactiae C;Date: 31-Dec:193 #sequence_revision 02-Aug-1994 #text_change 15 C;Accession: S33851; S32631
                                                                                                                                                                                                                                          A;Cross-references: GB:AE001180; GB:AE000783; NID:g2688755; A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                                                                                                                   C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: C70203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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  457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 NTIDVTIPQGYGSYN-----SFSINYKTKIT----NEQQKEFVNNSQAWYQEH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 IEWNLDKNQFGAKVRIQRSGSWILGVRPGDLKVLKFERD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 GKEEVNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 QTMTWDIEAVKKDPYVVQIRGGYLGTVFSKNGGWIDIEEATKLGIEIIFSGQKLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 NINYNAGGSRTDSV-YAKSGVLDDFDSTGRIVNWYFNFNAALNPI-KDEDVEFMTTDNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 NVTVHKSEAGTSSVFYYKTGDMLPEDTTH--VRWFLNINNEKSYVSKDITIK----DQIQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 GGQQLDLSTLN----INVTGTH-SNYYSGQSAITDFEKA-----FPGSKITVDNTK 126
IKKGDTFSIVKMKTSEHETKAPFRYTEASLVQKMEKEGIGRPSTYSTI---ISTLLEREY 513
                                             ITSGNKSTNVTVHKSEAGTSSVFYY------KTGDMLPEDTTHVRWFLNINNEKSY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IKIPK-WTNYNGLIPYVKPLNQTSISVKLTAKITEKTMRDQTIEYVENDSIPKIEG
                                                                                                                      Similarity
                                                                                                                                                                                                                   bacterial type I DNA topoisomerase
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                                                                                               Conservative
                                                                                                                   8.6%;
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                                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches
                                                                                                                 Score 96.5; D
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                                                                                                                                                                                                                                                                                                                                                                                                             spirochaete,
                                                                                                                                             DB 2;
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                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85;
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                                                                                                                                             Length 848;
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                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi.
                                                                                                                                                                                                                                                                   PIDN:AAC67161.1; PID:g268
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                                                                                                  75;
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                                                                                             Gaps
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                                                                                               14;
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finger protein MSN2 - yeast (Saccharomyces cerevisiae)
N,Alternate names: protein YM9532.02c; protein YMR037c
C;Species: Saccharomyces cerevisiae
C;Date: 15-oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: S39004; S52886; A48131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 269, 11987-11992, 1994
A;Title: Conserved domain structure of beta-neurexins. Unusual cleaved signal sequences A;Reference number: A53580; MUID:94216308
A;Accession: A53580
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A;Molecule type: mRNA
A;Residues: 1-392 <USH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurexin III beta precursor (clone pB794-7) - bovine C;Species: Bos pringenius taurus (cattle) C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 17-Mar-1999 C;Accession: A53580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A53580
 A;Reference
                    submitted
                                    R;Odell,
                                               A; Cross-references: EMBL:L08838; NID:g349594; PIDN:AAA34806.1;
                                                                   A; Molecule type: DNA
A; Residues: 1-704 <EST>
                                                                                                      A; Reference number: A48131;
A; Accession: S39004
                                                                                                                                       A; Title: Two homologous zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:L27864
                                                                                                                                                        Estruch, F.; Carlson,
ol. Cell. Biol. 13, 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                     199 NTDNERFQMVKQKIPFKYNRPVEEWLQEKGRQ-----LTIFNTQAQIAIGGKDKGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 IEGTVKG---ELKVLKQDK 208
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                                  c.;
to the EMBL Data Library, February 1995 ce number: S52885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFLN----INNEKSYVSKDITIKDQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                        NVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSIN--YKTK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEHHFHGSK------HHSVPISIYRSPVSLRGGHAGATYIFGKSGGLIL-----YT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                  Bowman, S.
                                                                                                                   13, 3872-3881, 1993
cologous zinc finger genes
er: A48131; MUID:93309420
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Pred. No.
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                                               PID:g349595
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                                                                                                                                     suppression
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A;Accession: S52886
A;Molecule type: DNA
A;Residues: 1-704 <ODE>
A;Cross·references: EMBL:Z48502; NID:g695715; PIDN:CAA88403.1; PID:g695717; GSPDB:GNO
C;GenetLos:
A;Gene: SGD:MSN2; MIPS:YMR037c
A;Gene: SGD:S0004640; MIPS:YMR037c
A;Cross-references: SGD:S0004640; MIPS:YMR037c
C;Cups-references: SGD:S0004640; MIPS:YMR037c
C;Superfamily: finger protein MSN2
C;Superfamily: finger protein MSN2
C;Superfamily: finger protein MSN2
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger F;649-665/Region: zinc finger CCHH motif
F;678-698/Region: zinc finger CCHH motif
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                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005176; NID:g12723558; A;Experimental source: strain IL1403 C;Genetics:
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E86706
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                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. in press, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Bolotin, A.; Wincker, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: E86706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 RRFSDV-ITNQFPSMTNSRNSISHSLDLWNHPKINPSNRNTNLNIT-TNSTSSSNASPNT 342
                                                                                                     76
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                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                 ITSGNKS---TNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITI 75
                                                           KTDAEGIKKGDIVTIKVKRKPTNILGVYIMSGNVQSKKSNIKQHSKS--NNEPSNSNTKK
                                                                                                KDQIQGGQQLDLSTLNI-----NVTGTH----SNYYSGQSAITDFEKAFPGSKITVDNTK- 126
                                                                                                                                          LTYMNSSPDYTSVSVFKKDLDDDKNVVGKTFEFKVTDRTETS--INADDEISF----FTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DL-VNKQDEDPK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMTKINPSQQLQQQLNRVQHKQLTSSHNNSSTNMKSFNSDLYSRRQRASLPIIDDSLSY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYKTKITNEQQ-KEFVNNSQ--AWYQEHGKEEVNGKSFNHTVHNINANAG---IEGTVKG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTMNANADSNI-AGNPKNNDATIDNELTQILNEYNMNFNDNLGTSTSGKNKSACPSSFDA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFEKAFPGSKITVDNTKN---TIDVTIPQGYGSYN------SFSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DITIKDQIQG------GQQLDL-----STLNINVTGTHSNYYSGQSAIT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDTNSYSNSISNSNSNSTGNLN----SSYFNSLNIDSMLDDYVSSDLLLNDDDDDTNLSR
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                                                                                                                                                                                                                        58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
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21.7%;
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25.4%;
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                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                                                             Score 95; I
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Pred. No.
-NTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV 160
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                                                                                                                                                                                                                        ; 68
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                                                                                                                                                                                                                                                               Length 359;
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                                                                                                                                                                                                                        84;
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A; Molecule type: DNA
A; Residues: 464-2020 <MOS>
A; Residues: 464-2020 <MOS>
A; Cross-references: GB:D85081; NID:g3041754
A; Cross-references: GB:D85081; NID:g3041754
A; Experimental source: strain K-12
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:88099, NCBIP:88090)
R; Blattner, F R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                           ABC-type transport protein ydbA.2 - Escherichia coli
(;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 08-Oct-1999
C;Accession: C48399; D64891; H64891
R;Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
A;Reference number: A48399; MUID:92190338
A;Accession: C48399; MUID:92190338
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C48399
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J. Bacteriol. 174, 1619-1625, 1992
A;Title: Cloning and sequence analysis of the muramidase-2 gene from Enterococcus hirae.
A;Reference number: A42296; MUID:92165737
A;Accession: A42296
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus hirae (ATCC 9790) C;Species: Enterococcus hirae C;Species: Enterococcus hirae C;Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #text_change 15-Oct-1999 C;Accession: A42296
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A; Residues: 1-666 < CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 TSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTH-----VRWFLNINNEKSYVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDITIKDQIQGGQQLDLSTLNI------NVTG-THSNYYSGQSAITDFEKAFPGSKITV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHNINANAGIEGTVKGELKVLKQDKDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVHNINANAGIEG-TVKGELKVLK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSGDSVWKIANDHG-----ISMNQLIE-WNNIKNNFVYPGQQLVVSKGSSSASGSTSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSGNSGGSATT----TGTTYTVKSGDSV-WGISHSFGITMAQLIEW-NNIKNNFIYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------NN-----SQAWY--QEHGKEEVNGK-----SFNHT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSGDKFSKNYEGDFNNLLDSIKYTKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLKNTTSNNMSDFTATNETEGSSSESYAWYISLKQNEEKYNGEMVVLDVDGGIISFTIY 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%;
24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                            Riley,
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C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: C71953
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Tves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V
Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-839; LDELYFQTSVIT' <BLA1>
A; Cross references: GB.AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1;
A; Experimental source: strain K-12, substrain MG1655
A; Accession: H64891
                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-2902 <ARN>
A;Cross-references: GB:AE001464; GB:AE001439; NID:g4154789; PIDN:AAD05855.1; PID:g415
A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric A; Reference number: A71800; MUID: 99120557 A; Accession: C71953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Molecule type: M',915-2020 <BLA2>
A;Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: ydbA_2
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: D64891
A;Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin-like outer membrane protein jhp0274 – Helicobacter pylori (strain J99)
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                            1335 NLSQNASINASNHSTLEL----QGDLNLNDTSS----LNLNQSAINVSNNATINDYASLI 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 VNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 ATVDN-KGTMTVTDPESMGIQIDGDKAIVNNEGESTITNGGTGTQINGDDATANNNGKTT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 NGELVITGDNATVNNNGKTTVDGKDSTGTEINGNNGK-VIQDGDLDVSGGGHGIDITGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 TLTIRDSVFTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSADGATKWQYNH
    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GQQL----DLSTLNIN------VTGTHSNYYSGQSAITDFEK------AFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 HHHRNNSPLPPTPPDDESDDTPVPPTPGGDEIIPDDPDDTPTPPKPVSFNNDVILDKTEK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                        23 NKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GTS---SVFYY---KTGDMLPEDTTHVRWFLNI-----NNEKSY--VSKDITIKDQIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 нннннн-----
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  IQGGQQLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDGKDSTGT--EINGNNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITVDNTKNTIDVTIPQGYG---SYNSFSINY--KTKITNEQQKEFVNNSQAWYQEHGKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
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                                                                                                                                      Conservative
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25.1%;
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23.1%;
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  -LSTLNI----
                                                                                                                                  Score 94.5; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 95; DB
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVI-QDGD 354
  ----NVTGTHSNYYSGQSAITD- 110
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                                                                                                                                                                              Length 2902;
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                                                                                                                                      Indels
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                                                                                                                                      77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vovis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith,
                                                                                                                                      11;
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Sear Job	Дb	Qy	Db	Qy	Db
ch con	1492	161	1447	111	1387
Search completed: January 30, 2002, 00:03:33 Job time: 2551 sec	1492 -NSQLVESDQGSLNIANIDLLSDLNGNKNRVYNI 1524		1447 TAFNFYDNAFSQSPITEHQALDIKVPLSLGGNLLNPNNSSVLNLK 1491	111FEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFV 160	:   387 ASNGSHLNENGAVNENSANITTSLSSSSIVEKGAVSLRGQENLSNNSSLDEQGSSAITSN 1446

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                     1122
1054.5
904
830
-178
165.5
125.5
114.5
                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                     100.0
94.0
80.6
74.0
15.9
14.8
11.2
10.3
10.3
                                                                                                                                                                                                                              Match
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113:
113:
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21:
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1122
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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Copyright (c) 1993 - 2000 Comp
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
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 1185
159
458
146
345
473
688
2032
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                   AAB37668
AAW31555
AAW68400
AAY00241
AAY00238
                                                                                                              AAW31554
AAW31554
AAR22675
AAW31552
AAB37667
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                                 Collagen binding p
Collagen binding p
Collagen binding p
Collagen binding p
Collagen binding A
Collagen binding A
Collagen binding A
Firbonectin-bindin
Clostridium botuli
Enterococcus faeca
                                                                                                                                                                                                                          Description
Enterococcus faeca
Enterococcus faeca
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Enterococcus hirae	AAR85291	17	666	8.5		45
Human membrane-ass	AAB29654	21	667		96	44
н	AAW44778	19	329			43
Staph. epidermidis	AAY70119	21	1802		<u>ه</u>	42
Cell wall protein	AAY83170	21	1802		٠	41
S. epidermidis ope	AAG82343	22	1155	8.6	9	40
	AAW68398	19	451		97	39
Nucleotide sequenc	AAW37738	19	437	•	97	38
	AAW59053	19	195		7	37
Fibroblast growth	AAW56000	19	351	8.8	98.5	36
Human apoAIV mutei	AAR39493	14	346		œ	35
N. meningitidis Z2	AAU06180	22	592		ō.	34
N. meningitidis P2	617	22	589		ø.	33
A surface protein	AAY23745	20	589	•	99.5	32
Haemophilus influe	AAB01846	21	1536		100	31
Haemophilus high m	AAR63505	15	1536	٠	100	30
High molecular wei	AAR41725	14	1536	•	100	29
High molecular wei	AAR41723	14	1536		100	28
Haemophilus influe	4	21	1095	8.9	100	27
Sequence of the As	AAP60452	7	537	•	100	26
Non-typeable Haemo	AAW30292	18	1601	•	101.5	25
Class A starch bra	AAW06400	17	847	9.0	101.5	24
·Firbonectin-bindin	AAW31556	19	139	•	103.5	23
High molecular wei	AAR41732	14	1529		104.5	22
	AAR39498	14	342		105.5	21
ω	AAW30293	18	1536		0	20
M. catarrhalis les	AAB69136	22	2314		110	19
P. falciparum spor	AAR13992	12	493	9.8	110	18
Non-typeable Haemo	AAW30291	18	1598		110.5	17
High molecular wei	AAR41731	14	1338	9.8	0	16
	AAB61673	22	184	10.1	ω	15
Human KGF-2 constr	AAB10309	21	184	10.1	w	14
E.coli optimised K	AAY32917	20	184	10.1	113.5	13
Enterococcus faeca	AAY00242	20	2032	10.2	114.5	12

## ALIGNMENTS

RESULT AAW31553

21-MAY-1998 (first entry)

AAW31553;

AAW31553 standard; Protein;

211 A

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Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRANM; adhesin; vaccine; immunisation; diagnosis; therapy; epitope M31.
       (UABR-) UAB RES FOUND.
(TEXA ) UNIV TEXAS A & M SYSTEM.
                                                       14-MAY-1997;
                                                                          20-NOV-1997
                                                                                                                          Protein
                                                                                                                                                                        Staphylcoccus
                                                                                                                                                                                                                                          Collagen binding protein M31 epitope
                                    16-MAY-1996;
                                                                                             W09743314-A2
                                                                                                                                            Peptide
                                                                                                                                                                         aureus.
                                    96US-0017678.
                                                       97WO-US08210
                                                                                                                          /note= "vector pQE30-derived peptide"
13..211
                                                                                                                                                    Location/Qualifiers
                                                                                                                /note= "epitope M31"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This protein comprises Staphylococcus aureus collagen binding CC protein (CBP) epitope M31, i.e. amino acids 61-343 of full-length CC BP, plus a vector-derived N-terminal peptide. Claimed 441, 849 CC and 1500 bp nucleic acid sequences (see AAT93436-38) respectively ce encode CBP epitopes M17, M31 and M55 (see AAW31552-54) that confer CC protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP cepitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in composition and methods for the prevention of composition in an animal such as a human. The CBP concerns are also contemplated for use in the preparation of concerns and as carrier proteins in vaccine formulations, as well as in the formulation of compositions for the prevention of s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
 Key
Peptide
                                                                                    Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-008801/01.
N-PSDB; AAT93437.
                                             Staphylcoccus
                                                                         epitope M55.
                                                                                                                                                  Collagen binding protein M55 epitope
                                                                                                                                                                                                                                         AAW31554 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31; Page 115-116; 143pp; English.
                                                                                                                                                                               21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aureus infection.
                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL
                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                     TVDNTKNTIDYTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      NHTVHNINANAGIEGTVKGELKVLKQDKDTK 211
                                                                                                                                                                                                                                                                                                                                                                            tvdntkntidvtipqgygsynsfsinyktkitneqqkefvnnsqawyqehgkeevngksf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mrgshhhhhhgsddkvatitsgnkstnvtvhkseagtssvfyyktgdmlpedtthvrwfl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                             aureus.
Location/Qualifiers
1..12
                                                                                                                                                                                                                                           Protein; 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1122; DB 19;
Pred. No. 1.2e-86;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sthanam N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Symersky J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211;
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                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (CBP) epitope M55, i.e. amino acids 30-531 of full-length CC CBP, plus a vector-derived N-terminal peptide. Claimed 441, 849 cc and 1500 bp nucleic acid sequences (see AAT93136-38) respectively cc encode CBP epitopes M17, M31 and M55 (see AAW31552-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP cepitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in composition and methods for the prevention of bacterial colonisation in an animal such as a human. The CBP carrier also contemplated for use in the preparation of contemplated for use in the preparation of sein the formulation of compositions for the prevention of S.
                                                                                                                                                                                                                                                                                                                            Matches 211;
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody that interacts with collagen binding Staphylococcal cna gene product - useful to put a named infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 31; Page 117-119; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΨPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UABR-) UAB RES FOUND (TEXA ) UNIV TEXAS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9743314-A2
                                                                                                                                            121 ltqtntsddkvatitsgnkstnvtvhkseagtssvfyyktgdmlpedtthvrwflninne
                                                                                                                                                                             12
                                                                                                                                                                                                        61
                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                              1 MRGSHHHHHHG-----
                                                                                  1998-008801/01.
                             kntidvtipggygsynsfsinyktkitnegqkefvnnsqawygehgkeevngksfnhtvh
                                          KNTIDYTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVH
                                                                                                                  KSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNT
                                                                                                                                                                             ----SDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNE
                                                                                                                                                                                                       ptsgtvkiegysktvpltvkgeqvgqavitpdgatitfndkveklsdvsgfaefevqgrn
                                                                                                                                                                                                                                                                 mrgshhhhhhgsardisstnvtdltvspskiedggkttvkmtfddkngkiqngdmikvaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV TEXAS A & M
                                                                                                                                                                                                                                                                                                                                                                                                   512 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0017678
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                                                                                                                                                                                                                                                                                                                                         94.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus collagen M55, i.e. amino acids 30-531 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "epitope M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "vector pQE30-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patti JM,
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                         Score 1054.5; DB
Pred. No. 1.8e-80;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sthanam
                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevent bacterial sepsis
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                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
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                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                   Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Of.
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                                                                                                                                                                                                                                                                                                                            115;
                                                                                                                                                                                                                                                                                                                           Gaps
                              300
                                                          185
                                                                                       240
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                                                                                                                                                                             65
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RESULT ANAELZ675
ID ARZ 2675
ID ARZ 2675
AX ARZ
XX ARZ
XX ARZ
XX CBP;
XX Regi
FT SW1
FT SW1
XX CBP;
XX
                The amino acid sequence (encoded by the sequence assembled from partially homologous pl6 and cCOLR6A inserts) comprises a structure resembling a signal sequence. Following this region, a region called A is found followed by a repetitive stretch of 187 amino acids called B1, B2 and B3. Directly following these regions there is a region called W which consists of a repetitive, hydrophilic
  structure contg. several proline residues.
                                                                                                                                                                                                                                                    Hybrid DNA molecule encoding S.aureus collagen binding protein protein is expressed in E.coli and used for diagnosis e.g. of
                                                                                                                                                                                                                                                                                                                              WPI; 1992-167099/20.
N-PSDB; AAQ24123.
                                                                                                                                                                                                                                                                                                                                                                                               Guss BM, Hook M,
Switalski LM;
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                                                                                                                                                                                        Disclosure; Fig 2; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALFA ) ALFA LAVAL AGRI INT AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding protein; mastitis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90SE-0003374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-SE00207
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1180..1185
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1160..1179
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/label= W
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30..1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label-
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                                                                                                                                                                                                                                                                                                                                                                                                                       Jonsson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .908
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                                                                                                                                                                                                                                                                                                                                                                                                                       Lindberg KM,
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This region
                                                                                                                                                                                                                                                                                                                                                                                                                       Patti J,
                                                                                                                                                                                                                                                                                                                                                                                                                       Signaes LC;
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RESULT

AAW31552

ID AAW3

XX AAW3

AC AAW3

AC AAW3

AC CO11

XX CO11

XX CO11

XX CO11

XX CO11

XX EFT CO11

XX EFT Pept

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FT Prot

FT Prot

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to mediate the binding of the protein to the cell wall. The amino acid sequence nearest to the C-terminal end consists of a long stretch of hydrophobic residues followed by some charged amino acids This region is called M.

The CBP can be used for immunisation pref. in combination with a fusion protein, e.g. for vaccination of ruminants against mastitis caused by staphylococcal infections. It can also be used to block infection in an open skin wound, e.g. for blocking protein receptors or by immunisation. In the latter, the host produces specific antibodies which block the adherence of the bacterial strains to damaged tissue. This treatment can be used for septic arthritis membranes. Dosage for immunisation is 0.5-5 microg CBP/kg; for topical admin. the protein is used at a concn. of 25-250 microg/ml.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen binding protein M17 epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31552 standard;
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                        (UABR-) UAB RES FOUND.
(TEXA) UNIV TEXAS A & M SYSTEM
                                                                                                          16-MAY-1996;
                                                                                                                                                           14-MAY-1997;
                                                                                                                                                                                                                 20-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW31552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus.
                                                                                                       96US-0017678.
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13..159
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 2.4e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial colonisation in an animal such as a human. The CBI epitopes are also contemplated for use in the preparation of vaccines and as carrier proteins in vaccine formulations, as as in the formulation of compositions for the prevention of s
                                                                                                                                                                                                                                                 Collagen binding Ace protein; extracellular matrix-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bac in animal infected with Staphylococcus aureus
                     10-MAY-1999;
                                                                                                                                                                                                                                                                                                                      Collagen binding
                                                                10-MAY-2000; 2000WO-US12590.
                                                                                                                                                                                                        Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB37667 standard; protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                             16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                     99US-0133334
                                                                                                                                                                                                                                                                                                                      Ace protein
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96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 830; DB 19;
Pred. No. 2.7e-62;
D; Mismatches 0;
                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                              antibacterial; immunostimulant; vaccine;
protein; lamin binding; bacterial infecti
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of S.
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                Collagen binding Ace protein; extracellular matrix-binding p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This protein is an extracellular matrix-binding protein, which can bind with collagens such as collagen type 1 and type IV and with lamins. Ace protein can be used to inhibit attachment of enterococci to collagen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New collagen-binding protein from Enterococcus, useful e.g. in protective vaccines, for diagnosis and treatment of Enterococcal infections and for screening for compounds that inhibit collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TEXA )
                                                                                                                                                             10-MAY-2000;
                                                                                                                                                                                                                                                                        WO200068242-A1
                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen binding Ace protein collagen binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB37668 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is collagen binding Ace protein from Enterococcus faecalis, where Ace is adhesion of collagen from enterococcal bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26;
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                         (TEXA ) UNIV TEXAS A & M SYSTEM.
                                                                                                          10-MAY-1999;
                                                                                                                                                                                                                  16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEGTVKGELKV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-687639/67.
DB; AAC83828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rdkarftsfivrytstiteagqhqatfensydinyqlnnqdatnekntsqv-----knvf 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iadrqgsgqqlnkesftfdivndketky---islaefeqqgygkidfv--tdndfnlrfy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or prevent enterococcal infections, specifically as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pages 119-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kriekemeyer B,
ddy SR, Qin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                             2000WO-US12590
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                                                                                                          99US-0133334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owens RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weinstock
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Pred. No. 5.9e-07
3; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hook M, Murray BE;
                                                                                                                                                                                                                                                                                                                                                                                cerial; immunostimulant;
lamin binding; bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh
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                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
l infection
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis, where Ace is adhesion of collagen from enterococcal bacteria (see AAC83828 and AAB37667). Ace protein is an extracellular matrix-binding protein, which can bind with collagens such as collagen type I and type IV and with lamins. Ace protein can be used to inhibit attachment of enterococci to collagen and to treat or prevent enterococcal infections, specifically as a vaccine. The present sequence is the collagen binding domain of Ace protein.
                                                                                               W09743314-A2
                                                                                                                                       Key
                                                                                                                                                         Staphylcoccus
                                                                                                                                                                                      microbial surface MSCRAMM; adhesin;
                                                                                                                                                                                                         Fibronectin;
                                                                                                                                                                                                                           Firbonectin-binding MSCRAMM derivative pCF33
                                                                                                                                                                                                                                                21-MAY-1998
                                                                                                                                                                                                                                                                   AAW31555;
                                                                                                                                                                                                                                                                                      AAW31555 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to collagen binding Ace protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New collagen-binding protein from Enterococcus, useful e.g. in protective vaccines, for diagnosis and treatment of Enterococcal infections and for screening for compounds that inhibit collagen
         (UABR-) UAB RES FOUND.
(TEXA ) UNIV TEXAS A & M SYSTEM
                                      16-MAY-1996;
                                                          14-MAY-1997;
                                                                             20-NOV-1997.
                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rich RL, Kriekemeyer B,
Nallapareddy SR, Qin X,
                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                159 FVNNSQAWYQEHGKEEVNGKSFNHTVHNI 187
                                                                                                                                                                                                                                                                                                                                                                                               101 YYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKIT--NEQQKE 158
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                                                                                                                                                                                                                                                                                                                                                                           64 ky---islaefeqqgygkidfv--tdndfnlrfyrdkarftsfivrytstiteagqhqat 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSN 100
                                                                                                                                                                                                                                                                                                                                      fensydinyqlnnqdatnekntsq-vknv 146
                                                                                                                                                                                                                                                                                                                                                                                                                2000-687639/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterococci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                   pCF33; collagen binding protein; sepsis; infection; rface component regonising adhesive matrix molecule; esin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                          aureus.
                                     96US-0017678.
                                                          97WO-US08210
                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 165.5; DB 2
30.2%; Pred. No. 1.4e-06;
                                                                                                                  "vector pQE30-derived peptide"
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Weinstock GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Singh KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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ID AAW6
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Best Local Similarity
                                             Key
Peptide
05-MAR-1998
                                                                           Synthetic
                  WO9808540-A1
                                                                                    Clostridium
                                                                                                       botulism;
                                                                                                                                                        07-DEC-1998
                                                                                                                                                                            AAW68400;
                                                                                                                                                                                              AAW68400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                              167 kfynls 172
                                                                                                                                                                                                                                                                 158 EFVNNS
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                                                                                                                                                                                                                                                                 163
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microbial surface component regonising adhesive matrix molecule (MSCRAMM) derivative pCF33, plus a vector-derived N-terminal peptide. The invention relates to claimed nucleic acid sequences (see AAF93436-38) encoding S. aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see AAW31552-54) that confer protection against S. aureus infection. CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The epitopes are also contemplated for use in the preparation of vaccines and as carrier proteins in vaccine formulations, as well as in the formulation of compositions for the prevention of S. aureus infection. pCF33 and pDD (see AAW31556) were used to raise anti-MCFDAMM COLUMNIANA COLUMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum type G toxin C fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-008801/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hook M, House-Pompeo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Antitoxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-MSCRAMM polyclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 yvntk----ddvkatltmp-ayidpenvkktgnvtlatgigstta---nktvlvdyekyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 YYSGQSAITDFEKA---FPGSKITYDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mrgshhhhhhgsmvaadapaagtditnqltnvtvgidsgttvyphqagyvklny---gfs 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRGSHHHHHHGS----DDKVATITSGNKSTNV-----TVHKSEAGTSSVFYYKTGDM 48
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                                                                                                                                                                                                                                                                             botulinum
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                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotoxin;
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30.1%; Pred. No. 0.01;
                                                                                                                                                                                                                                                                       serotype G strain 113/30
"N-terminal His tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                              toxin G; intoxication; immunogen;
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RESULT
AAY00241
ID AAYC
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AC AAYC
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DT 20-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins are E. coli, insect cells and yeast cells. The recombinant toxins are used as immunogens for the production of vaccines and antitoxins that are useful in the treatment of hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the histidine-tagged C fragment of Clostridium botulinum (113/30 strain) type G neurotoxin, encoded by a DNA sequence (see AAV30596) in plasmid pETHISb. This vector can be used to express BotG soluble C fragment in Escherichia coli host cells, with the recombinant C fragment being purified on affinity column. The invention relates to recombinant proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat human and other animals at risk of intoxication with clostridial toxin
Enterococcus faecalis;
detection; attenuation;
                                                                                    20-APR-1999
                                                                                                                     AAY00241;
                                                                                                                                                     AAY00241 standard; Protein; 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from C. botulinum toxins, especially type B and type E toxins. Methods are provided which allow for the isolation of soluble recombinant proteins free of significant endotoxin contamination. Preferred hosts for production of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an affinity column. derived from C. bot
                                                Enterococcus faecalis antigenic polypeptide fragment EF124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV30596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230234/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thalley BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and animals at risk of intoxication with clostridial toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                                                                    VKGELKVLKQDK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINN 64
                                                                                                                                                                                                                                                                                                                                                                     tahqskfvv-----ydsmfdnfsinfwvrtpkynnndiqtylqneytiiscikndsgw 145
                                                                                                                                                                                                                                                                                                                                                                                                      TVDNTKNTIDVTIPQGYGS-YNSFSINY------KTKITNEQQKEF-----VNNSQAW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                   yisnissnailslsyrggrlidssgygatmnvgsdvifndigngqfklnnse----nsni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKSYVSKDITIKDQIQGGQQLDLS----TLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 120
                                                                                                                                                                                                                                                                                                                                       -YQEHGKE-----EVNGKS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hhhhhhhssghi----egrhmasma---------dtiliqvf---nn 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 376-378; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                 faecalis;
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%;
infection; vaccine; immune response; diagnosis;
; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 116; DB 17, Pred. No. 0.098;
                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                    ----FNHTVHNI---NANAGIEGT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        92
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AAY00238
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                                                                                                                                                             RESULT
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from Enteroclis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for acids. Products from the present invention can also be used for acids.
                                                                                                     AAY00238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1997;
06-MAY-1997;
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                                                                       20-APR-1999
                                                                                                                                  AAY00238 standard; Protein; 2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 230; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070095/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bailey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1998
                                                                                                                                                                                                         337
                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                                                     71 KDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKN-TI 129
                                                                                                                                                                                                                                                                                                                                                                                                           12 SDDKVATITSGNKSTNVTVHKS-EAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVS 70
                                                                                                                                                               10
                                                                                                                                                                                                      ddngdvvvdidhsgghatgtkgkiqlkktamd 368
                                                                                                                                                                                                                                                                                           DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG 177
                                                                                                                                                                                                                                                                                                                        ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl
                                                                                                                                                                                                                                    KSFNHTVHNINANAGIEGTVKGELKVLKQDKD
                                                                                                                                                                                                                                                                evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                                                                                                                 sydntasytnqgssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl 228
                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 25.5
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX20231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 AA;
                                                                       (first entry)
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        688;
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                                                                                                                                                                                                                                                                                                                           277
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Enterococcus faecalis; infection; vaccine; detection; attenuation; antigenic.

immune response; diagnosis;

Enterococcus faecalis protein EF123

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RESULT 1
AAY00240
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Best Local
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screen compounds to identify agonists and antagonists of E. faecalis p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide
                                                                                                                                                                                                                                                             1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
  detection;
                                                                                                    AAY00240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 224-225; 301pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bailey C,
                Enterococcus faecalis; infection; vaccine;
                                            Enterococcus
                                                                                                                            AAY00240 standard; Protein;
                                                                                                                                                                                                  1073 ddngdvvvdidhsgghatgtkgkiqlkktamd
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                                                                                                                                                                                                                                                                                                                                                                                                     12 SDDKVATITSGNKSTNVTVHKS-EAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents a protein isolated
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DB; AAX20228.
                                                                                                                                                                                                                               KSFNHTVHNINANAGIEGTVKGELKVLKQDKD
                                                                                                                                                                                                                                                          evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                     DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG
                                                                                                                                                                                                                                                                                                                   ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl 1013
                                                                                                                                                                                                                                                                                                                                                                          sydntasytnggssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl 964
                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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  attenuation; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2032
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                         faecalis protein EF124.
                                                                      (first entry)
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97US-0044031.
97US-0046655.
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                                                                                                                               2032
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 114.5;
Pred. No. 0.
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              immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
             diagnosis;
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RESULT 12
AAY00242
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Best Local S
Matches 54
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus antibodies in a sample acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
Enterococcus faecalis; infection; vaccine; detection; attenuation; antigenic.
                                                                                                                             AAY00242 standard; Protein; 2032 AA.
                                                                                                                                                                                                                                                           1014
                                           Enterococcus
                                                                                                                                                                                                  1073 ddngdvvvdidhsgghatgtkgkiqlkktamd 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 228-229; 301pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-1998;
                                                                      20-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                            908
                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                   965
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                                                                                                                                                                                                                                                                                                                                              71 KDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKN-TI 129
                                                                                                                                                                                                                                                                                                                                                                                           SDDKVATITSGNKSTNVTVHKS-EAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-070095/06.
                                                                                                                                                                                                                            KSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                        evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                      DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG
                                                                                                                                                                                                                                                                                                                 ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl
                                                                                                                                                                                                                                                                                                                                                                         sydntasytnqgssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl 964
                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                         faecalis
                                                                      (first entry)
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%;
25.5%;
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                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 114.5; D:
Pred. No. 0.91;
36; Mismatches
                                           EF125
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DВ

Length 2032;

vaccines ç

develop

93; 20;

Indels

29;

Gaps

9

70

1013

1072

immune response;

diagnosis;

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RESULT 13
AAY32917
ID AAY329
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Matches
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06-MAY-1997;
16-MAY-1997;
Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; globulin; total serum protein; blood; hypofibrinogenaemia; cirrl
                                                                                                                                                                                                             1073 ddngdvvvdidhsgghatgtkgkiqlkktamd 1104
                                                                                                                                                                                                                                                                           1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins can and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus antibodies in a sample of cacids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein activity.
                                              E.coli optimised KGF-2 mutant protein sequence.
                                                                              03-NOV-1999
                                                                                                                                       AAY32917 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 232; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
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N-PSDB; AAX20232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                908
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                                                                                                                                                                                                                                                                                                                                                                                                            SDDKVATITSGNKSTNVTVHKS-EAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVS 70
                                                                                                                                                                                                                                            KSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                    evttdnetgqqkivvkmahieapyymeyrslvtssaagstdtvsn-qvsitgngsevvhg
                                                                                                                                                                                                                                                                                                                                 ddvvitdtpspnqvldpeslvi--ygtn-----vtedgtitpdksvileegkdytl
                                                                                                                                                                                                                                                                                                                                                                KDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKN-TI 129
                                                                                                                                                                                                                                                                                                                                                                                             sydntasytnqgssrdvtgkvsiqhggesv--kkggeyhkddpdhvywhvmingaqs-vl
                                                                                                                                                                                                                                                                                                     DVTIPQGYGSYN-----SFSINYKTKITNEQ--QKEFVNNSQAWYQEHGKEEVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                             (first entry)
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114.5;
Pred. No. 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                  albumin;
                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                964
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QΥ

1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 60

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:: -- Query Match Best Local S Matches 45

Similarity

10.1%;

Score 113.5; Pred. No. 0.0

.045;

Conservative

35;

Mismatches

65;

Length Indels

47;

Gaps

9

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disease, nephrotic syndrome, trauma and crush injuries, gastrointestinal and lymphatic fistulae, and protein-losing gastroenteropathies. The methods can also be used to treat hypoglobulinaemia, total protein loss, damage to the sinus epithelium, and can be used to increase proliferation of epithelial cells of the bladder or prostate, stimulate proliferation of the salivary gland cells and to increase Goblet cell proliferation for
                                                                                                                                                                                            vasculitis, ulcerative bowel disease, serositis, subacute bacterial endocarditis, liver disease, amyloidosis, malnutrition, malignancy, congestive heart failure, constrictive pericarditis, cardiac valvular
                                                                                                                                                                                                                                                                                                                                                                                                                     gland cells, lacrimal gland cells, sinus epithelium, and Goblet cells. The methods can also be used to treat hypofilminogenaemia caused by a cirrhosis, and disseminated intravascular coagulation (DIC). The methods can be used to treat thrombocytopaenia and to alleviate hypoalbuminaemia. These diseases are caused by drug induced hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis; hypoalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia; hypoalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia; leukaemia, haemolytic syndrome; Zieve's syndrome; rheumatic disease; HELLP preeclamptic syndrome; congenital rubella syndrome; systemic lupus; Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy; infection; tissue necrosis; vasculitis; ulcerative bowel disease; serositis; subacute bacterial endocarditis; liver disease; amyloidosis;
Sequence
                                                                                                                                                                                                                                                                                                                                  thrombocytopaenia purpura, posttransfusion purpura, metastatic tumours in the bone, aplastic anaemia, myelofibrosis, leukaemia, haemolytic syndromes, cancer chemotherapy, Zieve's syndrome, sepsis, HELLP preeclamptic syndrome, megaloblastic anaemia peritonitis, congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          keratinocyte growth factor-2 (KGF-2). KGF-2 fragments and mutants used in the methods of the invention, for increasing the level of platelets, fibrinogen, albumin, globulin, and total serum protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of keratinocyte growth factor-2 to increase levels of platelets,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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Escherichia o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congestive heart failure; constrictive pericarditis; nephrotic sycardiac valvular disease; hypoglobulinaemia; keratoconjuctivitis
                                                                                                                                                                                                                                                                                        rubella syndrome, Epstein-Barr infectious mononucleosis, systemic lupus, preeclampsia, thyrotoxicosis, uraemia, rheumatic diseases, granulomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jimenez P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1998;
13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1999;
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                                                                                                                                                                                                                                                                 processes, bacterial viral and parasitic infections, tissue necrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelets, fibrinogen, albumin, globulin, and total serum protein in the
blood. KGF-2 can also be used to stimulate proliferation of salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibrinogen, albumin, globulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a deletion mutant of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-527359/44.
                                         or preventing
  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli
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98US-0074585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mendrick
                                         keratoconjuctivitis sicca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli optimised human
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypoalbuminaemia.
                                                                                                                                                                                                                                                                                        granulomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome; is sicca;
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RESULT 1
AB10309
ID AAB1
XX AAB1
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XX Huma
KW Huma
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KW Epit
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dermatological, gastrointestinal, hepatic, respiratory, renal and cerebroprotective activity. (I) is useful for stimulating epithelial cell proliferation in patients suffering from wound, mucositis, ulcer such as venous statis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful for treating inflammatory bowel disease, liver disorder, lung damage, diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
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28-FEB-1997;
13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               skin disorder; renal failure; brain injury; intestinal fibrosis; proctitis, female reproductive tract disorder; pulmonary fibrosis; pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; cytoprotective; dermatological; gastrointestinal; hepatic; respiratory; renal; cerebroprotective; mucositis; treatment; epithelial cell proliferation; inflammatory bowel disease; lung damage; liver disorder; diabetes; oral injury; gastrointestinal injury; liver disorder; diabetes; oral injury; gastrointestinal injury; gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft; gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;
                                                                                                                                                                                This invention describes a novel human keratinocyte growth factor, KGF-2 (I), which has antiuloer, antidiabetic, antilinflammatory, cytoprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-441307/38.
N-PSDB; AAA71215.
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                                                                                                                                                                                                                                                                          Example 7; Fig 15; 190pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-)
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23-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kgklygskefnndcklkerie---engyntyasfn------wgh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NINNEKSYVSKDITIKDQIQGGQQ------LDLSTLNINVTGT---HSNYYSGQSAITD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mrgshhhhhhgscqalgqdmvspeatnsssssfsspssagrhvrsynhlqgd---vrwrk
                                                                                                                                                                                                                                                                                                                                     keratinocyte growth factor useful for promoting and accelerating healing, comprising at least 10 contiguous amino acids from a fic amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duan DR,
Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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97US-0039045.
97US-0055561.
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97US-0910875.
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97US-0862432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retraction; hemopoietic syndrome; myelotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni J,
Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jimenez P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein SEQ ID
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, Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber JR;
Rampy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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RESULT 1
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Best Local Similarity
                                                         14-JUL-1999;
15-JUL-1999;
12-AUG-1999;
19-AUG-1999;
03-NOV-1999;
22-DEC-1999;
19-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder, renal failure, brain injury, breast tissue injury, urothelial damage, female reproductive tract disorder, intestinal fibrosis, proctitis, pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome and myelotoxicity. (I) is also useful for increasing the adherence of skin grafts to wound beds and to stimulate re-epithelialization from the wound bed, to produce changes in hepatocyte proliferation, to reduce the side effects of gut toxicity, to regenerate skin in full and partial thickness skin defects, and to prevent and heal damage to lungs. KGF-2 shows enhanced activity, increased stability, higher yield and better solubility. This sequence represents the human KGF-2 protein construct pQE60-Cys37 described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound; mucositis; ulcer; inflammatory bowel disease; liver disorder; lung damage; diabetes; oral injury; gastrointestinal injury; epidermolysis bullosa; renal failure; brain injury; proctitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB61673 standard;
                                                                                                                                                                                                                                                                                                         02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                               30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000; 2000WO-US18328
                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary fibrosis;
liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pQE60-Cys37 construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ngrqmyvalngk 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NINNEKSYVSKDITIKDQIQGGQQ-------LDLSTLNINVTGT---HSNYYSGQSAITD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGKE---EVNGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kgklygskefnndcklkerie---engyntyasfn----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lfsftkyflk--iekngkvsgtkkencpysileitsveigvvavkainsnyy---lamnk 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mrgshhhhhhgscqalgqdmvspeatnsssssfsspssagrhvrsynhlqgd---vrwrk 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
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                         99US-0148628.
99US-0149935.
99US-0163375.
99US-0171677.
2000US-0198322.
2000US-0205417.
2000US-9911224.
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                                                                                                                                                                                                                                             99US-0144024
                                                                                                                                                                                                                                                                                                         99US-0142343
                                                                                                                                                                                                                                                                             99US-0143648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemopoietic syndrome; ovary injury; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 113.5; DB 21; 23.4%; Pred. No. 0.045;
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human keratinocyte growth factor (KGF-2; see AAF31901 and AAB61657). The present sequence is a KGF-2 construct protein, which was generated in the present invention. KGF-2 can be used to stimulate epithelial cell proliferation in a patient, where the patient has a wound, mucositis, an ulcer, inflammatory bowel disease, liver disorder, lung damage, diabetes, oral injury, gastrointestinal injury, gut toxicity, epidermolysis bullosa, skin graft, skin disorder, renal failure, brain injury, breast tissue injury, urothelial damage, femmale reproductive tract disorder, intestinal fibrosis, proctitis, pulmonary fibrosis, peunrumonitis, plural retraction, haemopoletic syndrome, and myelotoxicity. In addition, KGF-2 can be used in the liver. KGF-2 also promotes internal healing, donor site healing, internal comments as a surgery in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A polynucleotide encoding the human keratinocyte growth factor useful for stimulating epithelial cell proliferation in a patients that has e.g a wound - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmetic surgery in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 15; 591pp; English.
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                                                                                                                                                                                         148 ngrqmyvalngk 159
                                                                                                                                                                                                                                                                    170 HGKE---EVNGK 178
                                                                                                                                                                                                                                                                                                                                           113 kgklygskefnndcklkerie---engyntyasfn-----
                                                                                                                                                                                                                                                                                                                                                                                                                      111 FEKAFPGSKITVD-NTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NINNEKSYVSKDITIKDQIQGGQQ------LDLSTLNINYTGT---HSNYYSGQSAITD 110 : | :: | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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Pred. No. 0.045;
35; Mismatches 65; Indels 47;
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Dillon PJ, Gentz RL;
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is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-856-253-8
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Query Match
Best Local Similarity
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Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 33, Appl	Sequence 92, Appl	•	Sequence 92, Appl	•	•	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appl1	Sequencé 10, Appl					

ALIGNMENTS

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GENERAL INFORMATION:
                                                                                                                                                                                                                 CLASSIFICATION: 514
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/017,678
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
PREPERENCE/DOCKET NUMBER: TAMK:193
                                                                                                                                 TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITCOMPATION COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TA TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. BO
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
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                                          TYPE: amino acid STRANDEDNESS:
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                     TOPOLOGY: linear
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House-Pompeo, Karen
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Score 1122; DB 4; Pred. No. 2.1e-94;

Length 211;

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							, ,	.no acid ISS: linear	TYPE: amino STRANDEDNESS: TOPOLOGY: li	TY: ST: TO: 10:	us;
						77 6: ds	I74-7577 ID NO: ISTICS: no acids	(512) 474 OR SEQ ID ARACTERIST 512 amino	TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 512 amino acids	TE INFORM SEQUI	
					лК:193	R: TAMK: ATION:	NUMBE CNFORM 418-	DOCKET NATION :	REFERENCE/DOCKET NUMBER: 720 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000	TELE	
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					/856,253 Herewith	£1y	MBER: US/08, Concurrently	N NUMBI	URRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: Concurren	CURRI API FII	
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					33	US/08856253		6 Application 1288214		ESULT 2 S-08-856-253: Sequence 6, Patent No. (	US RE
					DKDTK 211	ELKVLKO	GTVKGI	NANAGIE	NHTVHNI	181	Db
						ELKVLKO	GTVKG	NANAGIE	NHTVHNINANAGIEGTVKGELKVLKQDKDTK	181	. Qy
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	KI 120	FEKAFPGS FEKAFPGS	QSAITDI        QSAITDI	SNYYSG	NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 	)GGQQLI	IKDQIO	YVSKDIT	NINNEKS 	61 61	Qy Db
	ET 60	EDTTHVRW         EDTTHVRW	TGDMLPH	SVFYYK       SVFYYK	MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 	SGNKST	KVATI	HHHGSDI 	MRGSHHH        MRGSHHH	1 1	ф
0;	Gaps	0;	Indels	0;	Mismatches	0;	ative	Conservative	211;	Matches	~

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; MOLECULE TYPE: protein US-08-447-031A-2
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; TOPOLOGY: US-08-856-253-2
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Best Local Similarity
                                                                                                                                                            APPLICATION NUMBER: US/08/856,253
APPLICATION UMBER: US/08/856,253
APPLICATION 514
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGERENCE/DOCKET NUMBER: TAMK:193
TERFERENCE/DOCKET NUMBER: TAMK:193
TERFERENCE/DOCKET NUMBER: TAMK:193
TERFERENCE/DOCKET NUMBER: TAMK:193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HAPPLICANT: H
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COLLAGEN BINDING PITITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 DITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                     STRANDEDNESS:
                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston
                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
                                                                          159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.O. Box 4433
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Symersky, Jindrich
Symersky, Jindrich
BINDING PROTEIN COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        House-Pompeo, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hook, Magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arnold, White & Durkee
                                                                          amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Joseph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.4%; Score 1048; DB 2; 100.0%; Pred. No. 1.2e-86;
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US-08-856-253-7
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   Matches
             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local 9
                                                                                                                                                             REFERENCE/DOCKET NUMBER: TA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 47-7577
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: (FILING DATE: Concurre CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 345 amino acid
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60,
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKI 120
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   l Similarity
56; Conserv
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59; Conservative
                                                                                                                    amino acid
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                                                                                                                                   345 amino acids
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   Conservative
                                                                                        linear
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               11.2%;
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                                                                                                                                                                                                                                                                                                us 60/017,678
                                                                                                                                                                                                                                    33,928
   20;
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Score 125.5; DB Pred. No. 0.0009; 0; Mismatches 7
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Pred. No. 4.2e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF USE
                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                             DB 4;
   73;
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   Indels
                                Length 345;
   37;
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   Gaps
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RESULT 6
US-09-023-082A-30
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Sequence 30, Approximately No. 6077692
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                                                                 APPLICATION NUMBER: US 60,
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08,
FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
                                FILING DATE: 13-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 YVNTK----DDVKATLTMP-AYIDPENVKKTGNVTLATGIGSTTA---NKTVLVDYEKYG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 YYSGQSAITDFEKA---FPGSKITYDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NEW CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPEDTTHVRWF------LNINNEKSYVS-KDITIKDQIQGGQQLDLSTLNINVTGTHSN 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRUBER, JOACHIM R. DILLON, PATRICK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENTZ, REINER L.
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DUAN, D. ROXANNE
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05-JUN-1995
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               MBER: US 60/055,561
13-AUG-1997
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                                                                                                                                                                                                    US 60/039,045
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                                                                                      US 08/910,875
                                                                                                                                            US 08/862,432
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                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 184 amino acid
                                                                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                   ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser Tarre
                                                                         FILING DATE: 16-MAR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2001 Jer:
STREET: Bldg. 1
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 NGROMYVALNGK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 KGKLYGSKEFNNDCKLKERIE---ENGYNTYASFN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 FEKAFPGSKITVD-NTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                  APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 LFSFTKYFLK--IEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYY---LAMNK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NINNEKSYVSKDITIKDQIQGGQQ------LDLSTLNINVTGT---HSNYYSGQSAITD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGSHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGKE---EVNGK 178
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Berkstresser, Jerry W RATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Virginia
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                             16-MAR-1992
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High Molecular Weight Surface Proteins
of No. 5928651-Typeable Haemophilus
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                                                                                                                                                                                             US 08/302,832
                                                                            GB 9205704.1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                             APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
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LENGTH: 1338 amino acids
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                                      FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
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NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T---AKNGSDLTIGNASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGN 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVDNTKNTIDVTIPQGYGSY----
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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25.5%; Pred. No. 0.14;
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Best Local Similarity
                                  APPLICATION NUMBER: US 08/302,832
PRIOR APPLICATION DATA:
APPLICATION DATA:
US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BEIKSTRESER', JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STATE: Virginia
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                    TELEPHONE:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSDKVNITNQITIKAGVEGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKA----EI 794
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
: (703) 415-0810
(703) 415-0813
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25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stephen J
                                                                                                                                                                                                                                                                                            US/08/617,697
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Pred. No. 0.14;
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; TOPOLOGY: linear US-08-617-697-9
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US-08-728-470-10
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5928651
GENERAL INFORMATION:
                  TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1599 amino acids
                                                                                                                                                                                                                                    FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 16-MAR-1
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424 PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                         FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1112 DNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 1170
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TVDNTKNTIDVTIPQGYGSY---
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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STRANDEDNESS: single
                                                                                                                  NAME: Berkstresser, Jerry W REGISTRATION NUMBER: 22,651
                                                                                                                                                                            APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
                                                        TELEPHONE:
                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                      (703) 415-0810
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                                   415-0813
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                                                                                                                                                                                                                                                           US PCT/US93/02166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephen J
                                                                                                            22,651
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                                                                                               1038-633
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                  TELEFAX: (703) 415-08: INFORMATION FOR SEQ ID NO:
                                                NAME: Berkstresser, Jerry W
REGISTION NUMBER: 22,651
REFERENCE,DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042 NDNSTGLTISAKDYTVNNNYTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 1101
                                                                                                                                                    FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 VNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG----IEGT----VKGELKVLKQDKDTK 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker and Mattare, Ltd
                                                                                                                                                                        ИМВЕR: GB 9205704.1
16-MAR-1992
            415-0813
NO: 10:
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22.9%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                 US 08/302,832
                                                                                                                                                                                                                                                         US PCT/US93/02166
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                                                                                                1038-625 ·
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TYPE: amino acid STRANDEDNESS: si

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US-08-617-697-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08617697 Patent No. 5977336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atent No. 5977336 GENERAL INFORMATION:
                                                                                                                      TELEFAX: (703) 415-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,631
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 05-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US POFILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 NDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIK 110:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                929 TISSDKVNITNQITIKAGVEGGRSDSSEAENANLTIQTKELKLAGDLNISGFNKA----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 881 ITTNASGTQKTIINGNITNEKGDLNIKNIKADAEIQIGGNISQKEGN------L 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 VNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG----IEGT----VKGELKVLKQDKDTK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ITVDNTKNTIDVTIPQGYGSY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEKAFPGSK 119
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                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                            1600 amino acids
                                                                                                                                         (703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESS
                                                                                                                                                                                                                                                                                 JMBER: US PCT/US93/02166
16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Molecular Weight Surface Proteins of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                 US 08/302,832
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                                                                                                                                                                                                  1038-557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #1.30
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US-08-856-253-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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Best Local Similarity
                                                                                                            TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TATELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                         FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Concus
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ZIP: 77210
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                                    STRANDEDNESS:
                                                                                                                                                                                                         REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                        LENGTH:
                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                    amino acid
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Y: U.S.
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                                                                          139 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Arnold, Wh
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patti, Joseph M.
House-Pompeo, Karen
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                  linear
                                                                                                                                                  (512) 418-3000
                                                                                                                                                                                                                                                                                                                                              Concurrently Herewith
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                                                                                                                                                                                                                                                                                       US 60/017,678
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Query Match Best Local Similarity

9.2%; 25.7%;

Score 103.5; DB Pred. No. 0.025;

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Length 139;

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                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 415-08 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                               943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 18M FC COOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     997 TISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAK 1056
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                                                                                                                                                                   13
                                                                                       61 NINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVT-GTHSNYYSGQSAITDFEK----AF 115
                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 KYEHGGNIIDIDFDSVPHIHG -----FNKHTEIIEED ----TNKDKPSYQFGGHNSVD 119
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 2, Application US/08038682
No. 5549897
PGSKITVDNTKNTIDVTIPQGYGSYNSFSINYK----TKITNEQQKEFVNNSQAWYQEHG 171
                                                                                                                             NSKNLSITTNSSSTYRTI-----ISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGNL 996
                                                                                                                                                               DDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDM------LPEDTTHVRWFL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
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                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                               1536 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ST. GEME III, JOSEPH W
/ENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Shoemaker and Mattare, Ltd
On Tefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                     25.28;
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                                                                                                                                                                                                                       Score 100; I
                                                                                                                                                                                                    Pred. No. 1.5;
3; Mismatches
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Best Local :
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                                      1057
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino aci
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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APPLICATION NUMBER:
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OPERATING SYSTEM:
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                                                      PGSKITVDNTKNTIDVTIPQGYGSYNSFSINYK----TKITNEQQKEFVNNSQAMYQEHG 171
KEEVNGKSFNHTVHNINANAGI 193
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5603938-Typeable Haemophilus
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Db 1099 KVETSG-SNNNTEDSSDNNAGL 1119

Search completed: January 30, 2002, 00:02:24 Job time: 2907 sec

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

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SEQUENCE
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TRANSMEM
DOMAIN
                                                                           Kruhoeffer M., Cetin Y., Kaempf U., Forssmann W.-G.;
Submilted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

-i- EUNCTION: RECEPTOR FOR THE E.COLI HEAD-STABLE ENTEROTOXIN (E.COLI
ENTEROTOXIN MARKEDLY STIMULATES THE ACCUMULATION OF CGMP IN
MAMMALIAN CELLS EXPRESSING GC-C). ALSO ACTIVATED BY THE ENDOGENOUS
                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL
GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) (GUANYLYL CYCLASE C).
GUCY2C OR GUC2C.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                             PEPTIDE GUANYLIN.

CATALYTIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDV 131
                                                                                                                                                                                                                                                                                                                                                                                                         GIEGTVKGELKVLKQDKDTK
                                                                                                                                                                                                                                                                                                                                                                            GIEGTVKGELKVLKQDKDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDDKVATITSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M81736; AAA20874.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IPR001899; Gram_pos_anchor.
PS00343; GRAM_POS_ANCHORING; FAL:
Repeat; Transmembrane; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158
1178
151
533
1093
1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA;
         CONTAINS 1
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1183
1157
1177
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318
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                                                                                                                                                                                                                                                                                                                                                                343
                                                                                                                                                                                                                                                                                                                                                                                      211
         PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS.
B1.
B2.
B3.
MW; B6Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1048; DB 1;
Pred. No. 1.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYS/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLAGEN-BINDING.
3 X 187 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLAGEN ADHESIN
                                                                                                                                                                                   Craniata; Vertebrata; Hystricognathi; Cavii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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all; 3D-structure
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ID ATL_S
AC P5208
AC P5208
DT 01-0C
DT 20-AU
DE BIFUN
DE ANIDA
DE ACETY
GN ATL.
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Best Local
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         ATL_STAAU STANDARD; PRT; 1256 AA.
P52081;
P52081;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-2001 (Rel. 40, Last annotation update)
B1FUNCTIONAL AUTOLYSIN PRECURSOR [INCLUDES: N-ACETYLMURAMAL AUTOLSE (EC 3.5.1.28); MANNOSYL-GLYCOPROTEIN ENDO-BETA-N-ACETYLGLUCOSAMIDASE (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01094; ANE_receptor; Pfam; PF00211; guanylate_cyc; Pfam; PF00069; pkinase; 2.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z74734; CAA98989.1; -. HSSP; Q02846; 1AWL.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; Guanylt_cyclase.
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                                                                                                                                                                        334 LFGHMLKTFLRNG-ENTTAHKFAHAFRNLTFEGSTGPVTLDDSGDIDNTMVLLYTSVDTK
                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                             24 KSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTHVRWFLN-INNEKSYVSKDITIKDQIQGG 82 | 1::|: | | | :: | ::|
                                                                                                                                                                                                                                                   EKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAW----
                                                                                                                                                                                                                                                                             EELQKILKDPNRRSNVIVMCGTPQTMESLKIDWTATEDTVIILVDLFNNYYLEENATAP-
                                                                                                                                                                                                                                                                                                       QQLD---
                                                                                                                                                                                                                                                                                                                                 KASNLPFKSFSWNTSYVF--KNG----TESEHCFWYINALEAGVSYFSQVLGFKEMLRGN
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1 1 23
24 1076
24 433
434 457
458 1076
492 752
827 957
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82 82
191 191
198 198 198
198 287
287 287
306 306
310 348
360 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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19.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyc;
                                                                                                                                                                                                                                                                                                                                                                               %; Score 106; DB
%; Pred. No. 2;
37; Mismatches
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GUANYLATE CYCLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 1076;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                        392
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N-ACETYLMURAMOYL-L-ALANINE

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                                                                                                                                             Query Match
Best Local
                                                                            Matches
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REPEAT
REPEAT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                                                                                                                                                                            Pfam; PF01510; Amidase_2; 1. Pfam; PF01832; Amidase_4; 1. SMART; SM00047; LYZ2; 1.
                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ENDOHYDROLYSIS OF THE DI-N-ACETYLCHITOBIOSYL UNIT HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE
                                                                                                                                                                                                                                                                                                                            EMBL; D17366; BAA04185.1; EMBL; L41499; AAA99982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>:</del>
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                               Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foster S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oshida T., Sugai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RN450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95116542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium
                            790
                                                                                      Local
 60
                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - ((MAN)5(GLCNAC)2]-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE OLIGOSACCHARIDE IS RELEASED INTACT.

CATALYTIC ACTIVITY: HYDROLYSES THE LINK BETWEEN N-ACETYLMURAL RESIDUES AND L-AMINO ACID RESIDUES IN CERTAIN BACTERIAL CELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE N-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR LYTIC ENZYMES
                                                 KVATITSGNKSTNVTVHKSEAGTSSVF----YYKTGD-----MLPEDTTH---VRWF
 ----LNINN--EKSYVSKDITIKDQIQGGQQLDLSTLN-INVTGTHSNYYSGQSAITDFE 112
                          KIAQVKPNNTGIRASVYEKTAKNGAKYADRTFYVTKERAHGNETYVLLNNTSHNIPLGWF
                                                                              61;
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNDERGOES
                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                                                                                                                                                                 IPR002502; Amidase_2.
IPR002901; Amidase_4.
                                                                                                                                                                                                                                               Hydrolase;
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199
776
425
596
                                                                              Conservative
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775
1256
589
758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOLYTIC
                                                                                      8.7%;
21.6%;
                                                                                                                                             137384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Komatsuzawa H.,
                                                                                                                                                                                                                                              Signal;
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                                                                           39;
                                                                                                                                             MW;
                                                                          Score 98; DB
Pred. No. 9.5;
39; Mismatches
                                                                                                                                                                               BIFUNCTIONAL AUTOLYSIN.

- ACETYLMURAMOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
1.
                                                                                                                                                                                                                                             Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROCESSING
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                                                                                                                                            2BB76CAA292FDD20 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hong Y.-M.,
                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINK BETWEEN N-ACETYLMURAMOYL IN CERTAIN BACTERIAL CELL-WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO GENERATE
                                                                                                                                                                                                                                                                                                                                                                                                        as its content
                                                                                                     1; Length 1256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group;
                                                                            90;
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TOP1_BO
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15-DEC-1998
15-DEC-1998
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99,1.2) (OMEGA-PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    burgdorferi.";
Nature 390:580-586(1997).
-!- FUNCTION: THE REACTIO
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPA OR BB0828.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER. CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA, FOLLOWED BY PASSAGE AND REJOINING.
SUBUNIT: MONOMER (BY SIMILARITY).
MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, I.
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOS
AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMTLNQVAQIQAGLQYKPQVQRVPGKWTDAKFNDVKHAMDTK 1064
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(OMEGA-PROTEIN) (RELAXING ENZYME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848
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D.,
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PRINTS; PRO0417; TOPIAC; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMARR; SM00437; TOPIAC; 1.
SMARR; SM00436; TOPIBC; 1.
SMART; SM00493; TOPIBC; 1. InterPro; IPR002936; Toprim.
Pfam; PF01131; Topoisom\_bac; 1.
Pfam; PF01751; Toprim; 1. entities requires a license agreement (S or send an email to license@isb-sib.ch). use by non-profit institutions as long modified and this statement is not removed. entities requires a This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr InterPro; IPR000380; Pro\_topoisomrse. InterPro; IPR002936; Toprim. InterPro; IPR003601; DNAtopI\_ATP\_bind
InterPro; IPR003602; DNAtopI\_DNA\_bind AE001180; AAC67161.1; BB0828; -. institutions as long (See http://www.isb-sib.ch/announce/ as its content Usage γ̈ restrictions and EMBL ìs a collaboration for outstation in commercial no 9 its

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NVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVPWGTKNQVILTGNN----IAQGTFNATK

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RESULTATION OF SECULAR REPORT 
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Best Local
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MSN2_YEAST
P33748;
01-FEB-1994
01-FCT-1996
                                                                                                                                                                                    "The Saccharomyces cerevisiae zinc finger pare required for transcriptional induction response element (STRE).";
EMBO J. 15:2227-2235(1996)
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ZINC FINGER PROTEIN MSNZ (MULTICOPY SUPPRESSOR
M$N2 OR YMR037C OR YM9532 02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.

ISOMETASE; TOPOISOMERASE_IDNA-binding; Complete proteome.

ISOMETASE; TOPOISOMETASE; DNA-binding; Complete proteome.

ACT_SITE 324 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 848 AA; 97663 MW; 37DEA5FBLE12FA2C CRC64;
                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION. MEDLINE=96208509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                         Martinez-Pastor M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estruch F., Carlson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93309420; PubMed=8321194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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                                               FUNCTION: POSITIVE TRANSCRIPTIONAL FACTOR THAT ACTS AS A COMPONENT OF THE STRESS RESPONSIVE SYSTEM, RECOGNIZES AND BINDS TO THE STRESS RESPONSE ELEMENT (STRE) WHICH IS INVOLVED IN THE RESPONSE TO VARIOUS FORMS OF STRESS (HEAT, OXIDATIVE, OSMOTIC, ETC.).

INVOLVED IN THE REGULATION OF THE CTT1, DDR2, HSP12 GENES.
     SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologous zinc finger genes identified by multicopy suppression SNF1 protein kinase mutant of Saccharomyces cerevisiae."; Cell. Biol. 13:3872-3881(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEGTVKG---ELKVLKODK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  LOCATION: NUCLEAR TO MAMMALIAN EGR |
                                                                                                                                                                                                                                                                                                                         PubMed=8641288; T., Marchler G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                         Schueller C., Marchler-Bauer A.,
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EMBL; Z48502; CAA88403.1; -.
PIR; A48131; A48131.
PIR; S39004; S39004.
HSSP; P08047; 1SP1.
TRANSFAC; T01257; -.
SGD; S0004640; MSN2.
InterPro; IPR000822; Znf-C2H2.
InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; Zf-CZH2; 2.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; Znf-C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Nuclear protein; Zinc-finger;.
                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
MURAMIDASE-2 PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZN_FING
SEQUENCE FROM N.A.,
                                                      Bacteria; Firmicutes;
                                                                      Enterococcus hirae
                                                                                                                                                                      P39046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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DL-VNKQDEDPK 472
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                                                                                                                                                                                                                                                                                                                 NAMTKINPSQQLQQQLNRVQHKQLTSSHNNSSTNMKSFNSDLYSRRQRASLPIIDDSLSY
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                                                        Bacillus/Clostridium
SEQUENCE OF
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ASP-RICH (
C2H2-TYPE.
C2H2-TYPE.
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Pred. No. 6.
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                                                        Enterococcaceae,
                                                                                                 (PG-HYDROLASE-2)
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Query Match
Best Local S
Matches 49
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"Thermosensitive cell growth mutants of Enterococcus hirae that
elongate at non-permissive temperature are stimulated to divide by
parental autolytic enzymes.";
J. Gen. Microbiol. 139:3099-3117(1993).
--I. FUNCTION: MAY WORK IN CONCERT WITH AND POTENTIATE THE PROCESSIVE
HYDROLYTIC ACTION OF MURAMIDASE-1, WHICH REQUIRES BINDING OF THE
ENZYME TO NONREDUCING ENDS OF GLYCAN CHAINS. HYDROLYSIS IN THE
MIDST OF GLYCAN CHAINS WOULD INCREASE THE NUMBER OF BINDING SITES
                                                                                                                                                                                                                                           SIGNAL
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SMART; SM00047; LYZ2; 1.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The second peptidoglycan hydrolase covalently binds penicillin."; J. Bacteriol. 171:4355-4361(1989).
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002901; Amidase_4. InterPro; IPR002482; Lysm. Pfam; PF01832; Amidase_4; 1. Pfam; PF01476; Lysm; 6.
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MEDLINE-89327152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequence analysis of the muramidase-2 gene Enterococcus hirae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M77639; AAA24776.1;
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MEDLINE=92165737;
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                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOR MURAMIDASE-1. MAY FUNCTION IN FACILITATING SEPTUM FORMATION AND CELL SEPARATION. ACTIVE ON M.LUTEUS CELL WALLS AND ON E.HIRAE CELL WALL FRACTIONS, BUT NOT ACTIVE ON E.HIRAE INTACT CELL WALLS. CAN COVALENTLY BIND PENICULLIN.

CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN N-ACETYL-D-GLUCOSAMINE AND N-ACETYLMURAMIC ACID IN PEPTIDOGLYCAN HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.

SUBCELLULAR LOCATION: SECRETED.

DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES. SIMILARITY: CONTAINS 6 LYSM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                             A42296; A42296.
; P21697; 1PCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed.
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  Conservative
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607
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                    8.5%;
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LYSM 3.
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LYSM 6.
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LYSM 6.
                    Score 95;
Pred. No.
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  Mismatches
                                                                                                                                                                                                                                                                                  Signal.
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                                                                                                                                                                                                                                                                                                                                                                                         Kasal H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horiuchi T., Takeyohob DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
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STRAIN-KIZ / MG1655;

STRAIN-KIZ / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland !

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland !

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P3366; P76087; P76088; P76856; P76859; P76859; O1-FEB-1994 (Rel. 28, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 205; 9 KDA PROTEIN IN PAAY-ACPD INTERGENIC REGION.
                                                                                                                                                      ESCHETICHIA COLI K-12.";
BIOCHIMIE 73:1361-1374 (1991).
BIOCHIMIE 73:1361-1374 (1991).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENETHIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                        Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                   MEDLINE=92190338; PubMed=1665988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aiba H., Baba T., Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDBA OR B1401/B1405.
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSGDSVWKIANDHG-----ISMNQLIE-WNNIKNNFVYPGQQLVVSKGSSSASGSTSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSGNKSTNVTVHKSEAGTSSVFYYKTGDMLPEDTTH-----VRWFLNINNEKSYVS
                                                                                                                                                                                                                                                                                                                                                          464-2003 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD; PRT; 2003 AA P76088; P76856; P76857; P768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K., Hayashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Escherichia coli K-12. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
                                                                                                                                                                             (AC P25928).
THE GENE CODING
2D/IS30C ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isono K., Itoh
                                                                                                   a collaboration
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RESULT 6
BXG_CLOBO
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REMBL; D90778; BAA15009.1; ALT_SEQ.

REMBL; D90778; BAA18880.1; ALT_SEQ.

REMBL; D90779; BAA18881.1; ALT_SEQ.

REMBL; D90779; BAA18881.1; ALT_SEQ.

REMBL; D90779; BAA18881.1; ALT_SEQ.

REMBL; M262680; "; NOT_ANOTATED_CDS.

RECGGENE; EG11307; ydbA.

RECGGENE; EG11307; ydbA.

RECOMPLICT 495 495 1 -> V (IN REF. 2).

SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                            Campbell K., Collins M.D., East A.K.;

"Nucleotide sequence of the gene coding for Clostridium botulinum
(Clostridium argentinense) type G neurotoxin: genealogical comparison
with other clostridial neurotoxins.";
Biochim. Biophys. Acta 1216:487-491(1993).

-!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                            STRAIN=113 / 30;
MEDLINE=94092745; PubMed=8268233;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BOTULINUM NEUROTOXIN TYPE G PRECURSOR (EC 3.4.24.69) (BONT/G)
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                 BOTG.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q60393;
01-NOV-1997
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BXG_CLOBO
                                                                                                                                                                                                                                                                                                                                                                                                                 (BONTOXILYSIN G).
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             ENDOPEPTIDASE.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L)
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL AC
WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHAN
FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
 SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDGKDSTGT--EINGNNG-----KVI-QDGD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITVDNTKNTIDVTIPQGYG---SYNSFSINY--KTKITNEQQKEFVNNSQAWYQEHGKEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGELVITGDNATVNNNGKTTVDGKDSTGTEINGNNGK-VIQDGDLDVSGGGHGIDITGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQQL----DLSTLNIN------VTGTHSNYYSGQSAITDFEK-----AFPGSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHHRNNSPLPPTPPDDESDDTPVPPTPGGDEIIPDDPDDTPTPPKPVSFNNDVILDKTEK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHHHHHG-----SDDKVATITSGNK------STNVTVHKSEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATVDN-KGTMTVTDPESMGIQIDGDKAIVNNEGESTITNGGTGTQINGDDATANNNGKTT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTS---SVFYY---KTGDMLPEDTTHVRWFLNI-----NNEKSY--VSKDITIKDQIQG
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                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium group; Clostridiaceae;
SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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(BY
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                                CHANNEL
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                                                                                                                      P78032;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN)
UNITALISTING ENZYME) (SWIVELASE).
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METAL
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. STRAIN-ATCC 29342 MEDLINE-97105885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                      Mycoplasmataceae;
                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                  Mycoplasma pneumoniae.
                                                                                                               TOPA OR MPN261 OR MP572.
                                                                                                                                                                                                                              MYCPN
                                                                                                                                                                                                                                                                                     1004 YINKWFSITITNDRLGNANIYINGSLKKSEKILNLDR 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                       NCBI_TaxID=2104;
                                                                                                                                                                                                                TOP1_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M27.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurotoxin; Hydrolase;
                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                            944
                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                         838 DSIPFDLSLYTKDTILIQVF---NNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSD 894
                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 DMLP-----EDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLS----TLNINVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUTOTOXIN: TYPES A, B, Cl, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 VIFNDIGNGQFKLNNSE----NSNITAHQSKFVV-----YDSMFDNFSINFWVRTPKY
                                                                                                                                                                                                                                                                                                                                                                                                                             GTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGS-YNSFSINY-----
                                                                                                                                                                                                                                                                                                                                                                       -KTKITNEQQKEF-----VNNSQAW-YQEHGKE-----EVNGKS-----
                                                                                                                                                                                                                                                                                                                                            NNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYSIKDNISD 1003
                                                                                                                                                                                                                                                                                                                 ----FNHTVHNI---NANAGIEGTVKGELKVLKQDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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229
230
233
435
1296
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                             N.A.
                                                                                                                                                                                                                STANDARD;
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229
230
233
449
                                                                      Mycoplasma
                M129;
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23.0%;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOTULINUM NEUROTOXIN G, HEAVY-CHA
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
MW; DC8E47E15F665C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                 PRT;
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                                                                                   group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXIN G, LIGHT-CHAIN.

OXIN G, HEAVY-CHAIN.

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1296;
                                                                                     Mollicutes;
                                                                                                                                           (RELAXING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                            ENZYME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    943
                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                        179
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PubMed=8948633;

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RESULT 10
OPAH_NEIGO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01131; Topoisom_bac; 1.
Pfam; PF01751; Toprim; 1.
Pfam; PF01396; zf-C4_Topoisom; 2.
PF1NTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1AC; 1.
SMART; SM00437; TOP1AC; 1.
SMART; SM00433; TOPTBC; 1.
SMART; SM00433; TOPRIM; 1.
OPAH_NEIGO
Q04884;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).

-i- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-i- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000056; AAB96220.1; -.
HSSP; P06612; 1ECL.
InterPro; IPR003601; DNAtopI_ATP_bind.
InterPro; IPR003602; DNAtopI_DNA_bind.
InterPro; IPR000380; Pro_topoisomrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
Isomerase; Topoisomerase; DNA-binding; Zin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                495
                                                                                                                                                                                                                                                                                                                436
                                                                                                                                               197
                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                       54 THVRWFLNINNE-----KSYV------SKDITIK-DQIQGGQQLDLSTLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA, FOLLOWED BY PASSAGE AND REJOINING.
SUBJUNT: MONOMER (BY SIMILARITY),
MISCELLANDOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS FAMILY.
                                                                                                                AEGSIQRVKKEKE 618
                                                                                                                                             VKGELKVLKQDKD
                                                                                                                                                                              GEQVNEELSKHEGKIINKEFTKN-----MEKSLDEIAENKKNYQEFLRDFWSNEKEEVKL
                                                                                                                                                                                                              TKITNEQ------QKEFVNNSQAWYQEHGKEEV--NGKSFNHTVHNINANAGIE-GT 196
                                                                                                                                                                                                                                             TARQTHPAARYTQASLIEALEK---
                                                                                                                                                                                                                                                                            NVTGTH-SNYYSGQSAITDFEKAFPGSKITVDNTKNTI-DVTIPQGYGSYN--SFSINYK 148
                                                                                                                                                                                                                                                                                                              THIR-FINDGNKFYASSKSLVFDGYRKIYEHFENKESNDLYIDLDKIRVGDRFMAKDIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;; Complete proteome.

1G 624 652

1G 673 702

1TE 340 340

1CE 711 AA; 81965 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000380; Pro_topoisomrse. IPR002936; Toprim.
(Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             702 C
340 D
81965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analysis of the genome of the bacterium Mycoplasma
                                                                                                                                               209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rmatics Institute. There are no rest
institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                            8.2%;
                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plagens H., Pirkl E., Li B.-C
                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE 1.
C4-TYPE 1.
DA CLEAVACE (BY SIMILARITY).
, 16B86358BB06582E CRC64;
                                                                                                                                                                                                                                             -SNIGRPSTYNTMASVNLDRGYASLNKHAFHVTQL
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 711;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local S
Matches 45
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SEQUENCE FROM N.A.
STRAIN=MSI1 / F3;
STRAIN=MSI1 / F3;
MEDLINE=93178439; PubMed=8440254;
MEDLINE=93178439; PubMed=8440254;
Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
Kupsch E.-M., Knepper B., outer membrane proteins account for the cell
Kupsch E.-M., Knepper B., Weisseria gonorrhoeae for human leukocytes and
                                                                                                                                                                                                                                                                                          NON_TER
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, 15-DEC-1998 (Rel. 37, OPACITY PROTEIN OPA60
                                                                                                                                                                                                                                                             VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhat K.S., Gibbs C.P., Barrera O., Morrison Stern S., Kupsch E.-M., Meyer T.F., Swanson Mol. Microbiol. 6:1073-1076(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The opacity proteins of Neisseria encoded by a family of 11 complete Mol. Microbiol. 5:1889-1901(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhat K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F., Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MS11 / V18;
MEDLINE-92114767; PubMed-1815562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                       Outer membrane; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02462; Opacity;
                                                                                                                                                                                                                                                                                                                                                                                   PIR; S28631;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z18939; CAA79372.1; -. EMBL; X60711; CAA43121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92261323; PubMed=1584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
               113
                                            76
                                                                       58
                                                                                                  16
                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: IMPLICATED IN A NUMBER OF ADHIPROTEINS ARE IMPLICATED IN PATHOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: OUTER MEMBRANE.
-KAFPGSKI---
                                          KW----NNNKYSVNIE-NVRIRKENGIRIDRKTENQENGTFHAVSSLGLSAIYDFQINDK 130
                                                                                                                              SHHHHHHGSDDKVATITSGNKSTNVTVHKSEAGTSSVF-----YYKTGDMLPEDTTHVR 57
                                                                                                  AYAYEHITHDYPEPTAPNKNKISTVSDYFRNIRTRSVHPRVSVGYDFGGWRIAADYARYR 75
                                                                     -WFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFE----
                                                                                                                                                            45; Conserv
                                                                                                                                                                                                                                                                                                                                                                IPR003394; Opacity.
                                                                                                                                                                                                                               234
238
238
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                   S28631
                                                                                                                                                                                                                                    Ą,
                                                                                                                                                                                                                                                                                          >238
                                                                                                                                                                                                                            234 V -> M (IN MS11 / V18).
238
27073 MW; 883A3560C2DF1B9F CRC64;
-TVDNTKNTIDV-TIPQG--YGSYNSFSINYKTKITNEQQKEFVN 161:::::::| | | :::::
                                                                                                                                                                     8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta subdivision; Neisseriaceae;
                                                                                                                                                            35;
                                                                                                                                                         Score 91.5; D
Pred. No. 3.6;
Pred. No. 3.6;
                                                                                                                                                                                                                                                             OPACITY PROTEIN OPA60.
SED -> MLKA (IN MS11 / V18).
V -> M (IN MS11 / V18).
                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF ADHERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gonorrhoeae
genes.";
                                                                                                                                                                          3.6;
                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                            69;
                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain MS11 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARE
                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTIONS.
RE SUBJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jaehnig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'EJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria.
                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHASE
                                                                                                                                                           Gaps
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Query Match
Best Local Similarity
Thes 53; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUN_BACSP
P29019;
                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus sp. KSM-JJU., J. Gen. Microbiol. 137:41-48(1991).
J. Gen. Microbiol. 137:41-48(1991).
-I- FUNCTION: THIS ACID ENDOGLUCANASE IS ACTIVE OVER AN PROPERTY OF DH VALUES, BETWEEN 4.5 AND 6.5, WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOGLUCANASE PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE)
                                                                           SEQUENCE
                                                                                                               CHAIN
                                                                                                                                                     PROSITE; PS00812; GLYCOSYL_HYDROL_F8; 1. Cellulose degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 PROPEP
                                                                                                                                            SIGNAL
                                                                                                                                                                               Pfam; PF01270; Glyco_hydro_8; PRINTS; PR00735; GLHYDRLASE8.
                                                                                                                                                                                                                     EMBL; M68872; AAA22409.1;
PIR; A44808; A44808.
HSSP; P04955; ICEM.
                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                  + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Purification and properties of an acid endo-1,4-beta-glucanase from Bacillus sp. KSM-330.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ozaki K., Sumitomo N., Ito S.;
"Molecular cloning and nucleotide sequence of the gene encoding endo-1,4-beta-glucanase from Bacillus sp. KSM-330.";
J. Gen. Microbiol. 137:2299-2305(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELLULASE) (ENDO-K).

Bacillus sp. (strain KSM-330).

Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus group; NCBI_TaxID=1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92121880; PubMed=1770347;
                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 56-75, AND CHARACTERIZATION. MEDLINE=91259037; PubMed=2045781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: ONE TRP RESIDUE HAS BEEN PROVED TO BE THE MECHANISM OF ACTION OF ENDO-K.
SIMILARITY: BELONGS TO CELLULASE FAMILY D (FAMILY 8
                                                                                                                                                                                                                                                                                                                                                                                                                              LINKAGES IN CELLULOSE.
PTM: THE N- AND THE C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ENDOHYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                             HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH AT 5.2.
                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                       IPR002037; Glyco_hydro_8.
                                                                          56
130
191
463
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                        55
463
130
191
51882
                         8.1%;
21.2%;
                                                                           MW.
            31;
                        Score
Pred.
                                                                        ENDOGLUCANASE.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (POTENTIAL).
407FA54F5236C59E CRC64;
                                                                                                                             POTENTIAL.
                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus.
            Mismatches
                         91;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                               MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                                                              BE SUBJECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 1,4-BETA-D-GLUCOSIDIC
                                                                                                                                                                                                                                                                                                       There are no rest
                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
            64;
                                     Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5, WITH
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                TO BE INVOLVED :
                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                                                        읁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTREMELY
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            102;
                                                                                                                                                                                                                                                                                                                                                                                        GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPTIMUM
                                                                                                                                                                                                                                                                                                                                       collaboration
L outstation -
                                                                                                                                                                                                                                                                                                                                      outstation
          Gaps
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                                                                                                                                                                                                                                                                                                                         on
            13;
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RESULT 12
LIPA_MYCPU
ID LIPA_MAC
Q50274
AC Q50274
DT 20-AUG
CC Mycopl
RN [2]
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Q50274;
                                                                                                                                                                                                                                                                                                                                       "Mechanism of antigenic variation in Myc
site-specific DNA inversions.";
Mol. Microbiol. 18:703-714(1995).
-i- SUBCELLULAR LOCATION: ATTACHED TO TH
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STRALN=KD735-15;
MEDLINE=20245550; PubMed=10781561;
MEDLINE=20245550; PubMed=10781561;
Shen X., Gumulak J., Yu H., French C.T., Zou N., Dyt
"Gene rearrangements in the vsa locus of Mycoplasma
"Gene rearrangements in the vsa locus of Mycoplasma
J. Bacteriol. 182:2900-2908(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIPOPROTEIN A PRECURSOR.
                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRALN-UAB CTIP;
MEDLINE-21267165; PubMed-11353084;
Chambaud I., Hellig R., Ferris S., Ba
Moszer I., Dybvig K., Wroblewski H.,
                             EMBL; U23947;
                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                the European Bioinformatics Institute.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blanchard A.;
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SIMILARITY: BELONGS TO THE PULMONIS LIPAB LIPOPROTEIN FAMILY.
                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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SEQUENCE
                                                                                                        Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;

"Cloning of two new cry genes from Bacillus thuringiensis subsp.

wuhanensis strain.";

Curr. Microbiol. 40:227-232(2000).

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT

-!- EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PIERIS RAPAE.

-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                                                                                                                                                                                    CRYIG(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (133 CRYIGB OR CRYIG(B) OR CRYH2.
                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
PESTICIDIAL CRYSTAL PROTEIN CRY1GB (INSECTICIDAL DELTA-ENDOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein;
SIGNAL
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                          MEDLINE=20153386; PubMed=10688690; Kuo W.-S., Lin J.-H., Tzeng C.-C.,
                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID-52024;
                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis (subsp. wuhanensis). Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                      -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                        STRAIN-HD-525
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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N-ACYL DIGLYCERIDE (POTENTIAL).

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K -> S (IN STRAIN KD735-15).

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P28515;

01-DEC-1992 (Rel. 24, Create:

01-DEC-1992 (Rel. 24, Last s:

20-AUG-2001 (Rel. 40, Last a:

TRANSCRIPTION FACTOR ELT-1.
                           EMBL; X57834; CAA40967.1;
EMBL; Z68221; CAA92494.1;
PIR; A41267; A41267.
HSSP; P17678; IGAU.
                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch). ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91342668; PubMed=1875944;
Spieth J., Shim Y.H., Lea K., Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell.
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les 36; Conser
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTKITNEQQKEFVNNSQAWYQEHGKEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNTCESN--RGYGDYTPLPAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryonically expressed Caenorhabditis elegans to the GATA transcription factor family."; Biol. 11:4651-4659(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ELEYFPETDKVWI-EIGETE 1154
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conrad R., Blumenthal T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416
                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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WormPep; W09C2.1; CE03799

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RESULT LACZ THE LACZ 
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Best Local S
Matches 45
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2_THACU STAN
LAC2_THACU STAN
Q02075;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                   Wahleithner J.A., Xu F., Brown K.M., Brown S.H., Halkler T., Kauppinen S., Pederson A., Schneider The identification and characterization of four plant pathogenic fungus Rhizoctonia solani."; Curr. Genet. 29:395-403(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani). Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiales; Ceratobasidiaceae; mitosporic Ceratobasidiaceae; Rhizoctonia.
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Nuclear protein.
ZN_FING 217 241
ZN_FING 272 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=107832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACCASE 2
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                                                              FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).

CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE + 2 H(2)O.

CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE + COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

SUBCULT: HOMODIMER (BY SIMILARITY).

SUBCULTULAR LOCATION: SCREETED.

TISSUE SPECIFICITY: IN WYCELIA, AT A LOWER LEVEL THAN LCC4.

SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                            SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASSSSANSTSTPKNTISKANRSSG
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PS00344; GATA_ZN_FINGER_1; 2.
PS50114; GATA_ZN_FINGER_2; 2.
PSTO114; GATA_ZN_FINGER_2; 2.
     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 (Rel. 35, Created)
97 (Rel. 35, Last sequence update)
97 (Rel. 35, Last sequence update)
97 (Rel. 35, Last annotation update)
PRECURSOR (EC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)
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0320; GATA; 2.
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  Swiss
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44823 MW;
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SSVFYY  :  DYPFFY HSNYYS             	2000).  ; D5F9 ; Score Pred. 2; Mis	48146; ., Duh Ecoding a molecule	(FRAGMENT) ptococcus lus/Closti	Creat Last Last	PRT;	ALIGN	096266 Q9NDS4 Q9T069 Q9T291	Q99R42 Q9ZME6 Q99U53	052351 068170 09CHR9 09AI17	097260 097260 Q9KI14 Q28143	Q92HL0 Q973Q6 Q53971 Q99V41	Q9V9W0 Q9VJV6 Q9JPS5	Q9JPS8 Q48031 Q9JPI0 Q9JOW4
DMLPEDTTHV  :  :   :   DLAGE-SNQV AITDFEKAFP :: :    : SLAEFEQQGY	E0856A694 ; DB 2; ; 3.3e-06	W., Weinstock G., microbial surface, from different or production of a	ecalis). lium group;	iti oce	319 AA.	ALIGNMENTS		٠					
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01-MAR-2001
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09F863; O1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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MEDLINE=20407335; PubMed=10948146;

Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray E

"Diversity of ace, a gene encoding a microbial surface component
recognizing adhesive matrix molecules, from different strains of
entercoccus faecalis and evidence for production of ace during h
                                                                                                COLLAGEN
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Bacteria; Firmicutes;
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01-JUN-2001
       Enterococcus
                             Bacteria;
                                             Enterococcus faecalis (Streptococcus faecalis).
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EMBL; AF260873; AAG23932.1; -.
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PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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Bacillus/Clostridium group;
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STRAIN-MD9/TX0249;
MEDLINE-20407335; PubMed-10948146;
MEDLINE-20407335; PubMed-10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of enterococcus faecalis and evidence for production of ace during
  SECUENCE
                                                                                                                      MEDLINE=20407335; PubMed=10948146; Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray E "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of
                                                                        Infect. Immun. 68:5210-5217(2000).
EMBL; AF260872; AAG23931.1; -.
                                                                                                            enterococcus faecalis and evidence
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Pfam; PF00746; Gram_pos_anchor; 1.
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PROSITE; PS00343; GRAM_POS_ANCHORING;
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28.3%;
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Bacillus/Clostridium
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Pred. No. 1.2e-05;
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Query Match Best Local

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PARKER/TX2619;
MEDLINE=20407335; PubMed=10948146;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                           QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG 192
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                                                                                                                                                                                                                                                                                                                                                 IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
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ilarity 28.3%;
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a microbial surface component
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for production of ace during I
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STRAIN-B-343/TX2783;
MEDLINE-20407335; PubMed-10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface component "Diversity adhesive matrix molecules, from different strains or recognizing adhesive matrix molecules, from different strains or recognizing afacalis and evidence for production of ace during
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01-MAR-2001
01-MAR-2001
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STRAINS;
MEDLINE=20407335; PubMed=10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray
"Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray
"Diversity of ace, a gene encoding a microbial surface component
recognizing adhesive matrix molecules, from different strains of
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
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                                   enterococcus faecalis and
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Bacteria; Firmicutes;
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AF260895;
AF260880;
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AF260896; AAG23954.1; -.
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68:5210-5217(2000).; AAG23953.1; -.; AAG23938.1; -.
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Bacillus/Clostridium group;
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Bacillus/Clostridium group;
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3; Mismatches 88;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XBQ7;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                           Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rich R.L., Kreikemeyer B., Owens R.T., Weinstock G.W., Murray B.E., Hook M.; "Ace: a collagen-binding MSCRAMM from E J. Biol. Chem. 0:0-0(1999).

EMBL; AF159247; AAD43342.1; -.
HSSP; Q53654; IAMX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLLAGEN ADHESIN ACE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CG110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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  135
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                                                                                                                                                                      TITSGNKSTNVTVHKSEAG---TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT
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                                                                                                                                           TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGEASGNONV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
  QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEGTVKGELKV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDKARFTSFIVRYTSTITEAGOHQATFENSYDINYQLNNQDATNEKNTSQV-----KNVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                               IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY
                                                                                            IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP
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458
458 AA;
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                            458
51085 MW;
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                                                                                                                                                                                                                                                                15.9%;
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Bacillus/Clostridium group; Enterococcaceae;
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                                                                                                                                                                                                                                                                Score 178; DB 2; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 2;
Pred. No. 6.5e-06;
3; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                              B674692BD29A0A24 CRC64;
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                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                      Length 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  faecalis.
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RESULT
Q9F861
ID Q9
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DT 011
DT 01
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Best Local S
Matches 54
                                                                                            Q9F861 PRELIMINARY;
Q9F861;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-JUN-2001 (TrEMBLrel. 17, L
COLLAGEN ADHESIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9F862;
01-MAR-2001
01-MAR-2001
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STRAIN-LBJ-1/TX0020;
MEDLINE-20407335; PubMed-10948146;
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murra
Nallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murra
"Diversity of ace, a gene encoding a microbial surface compone
"Diversity of ace, a gene encoding a microbial surface compone
recognizing adhesive matrix molecules, from different strains
recognizing adhesive matrix molecules, from different strains
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SIGNAL
                                                                        ACE.
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Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inrect. Immun. 68:5210-5217(2000). EMBL; AF260878; AAG23936.1: -
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  Bacteria; Fiz
Enterococcus
                                                  Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGYGSYNSFSINYKTKIT--NEQQKEFYNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGEASGNQNV 300
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                                                                                                                                                                                                                                                                                                                                           VEGEASGNQNV
                                                                                                                                                                                                                                                                                                                                                                                        IEGTVKGELKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS
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                         Firmicutes;
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580 AA;
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1 (TrEMBLrel. 16,
1 (TrEMBLrel. 17,
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63948 MW;
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Bacillus/Clostridium grou
                      (Streptococcus faecalis). Bacillus/Clostridium grou
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Last
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Pred. No. 1.3e-05;
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7CD61EAD3FDA0993 CRC64;
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RESULT

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Q9F864; O1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                               Signal.
SIGNAL
                                                                                                                                                                                                                           STRAIN-MC02152/TX0024;

MEDLINE-20407335; PubMed=10948146;

Nallapareddy S.R., Singh K.V., Duh R.W.
"Diversity of ace, a gene encoding a mi recognizing adhesive matrix molecules, enterococcus faecalis and evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
SIGNAL
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                                                                          EMBL; AF260876; AAG23934.1;
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis
Bacteria; Firmicutes;
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EMBL; AF260879; AAG23937.L; .
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
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STRAIN-JH2-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
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68849 MW;
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Bacillus/Clostridium group; Enterococcaceae;
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POTENTIAL. ; C9B368AE30858359 CRC64;
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Pred. No. 1.3e-05;
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Best Local
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STRAIN-SESS/TXI329;
MEDLINE-20407335; PubMed-10948146;
Mallapareddy S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray B "Diversity of ace, a gene encoding a microbial surface component "Diversity adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules from different strains of recognizing adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules, from different strains of
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Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                          SEQUENCE
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EMBL; AF260875; AAG23933.1; -.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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                       IEGTVKGELKV
                                                RDKARFTSFIVRYTSTITEAGQHQATFENSYDINYQLNNQDATNEKNTSQV-----KNVF
                                                                         QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                                                                   IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY
                                                                                                                           IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP
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Pred. No. 1
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Pred. No. 1
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AFDC039BFD47C356 CRC64;
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Best Local
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01-MAR-2001 (TrEMBLrel. 16, C)
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-WH245/TX0635;
MEDLINE=20407335; PubMed=10948146;
MAILIAPAREDDY S.R., Singh K.V., Duh R.W., Weinstock G.M., Murray "Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of recognizing adhesive matrix molecules, from different strains of the strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BEB3/TX0855;
STRAIN-BEB3/TX0855;
MEDLINE-20407335; PubMed-10948146;
Nallapareddy S.R., Singh K.V., Duh R.W.
"Diversity of ace, a gene encoding a mirecognizing adhesive matrix molecules, recognizing adhesive matrix and evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9F858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                   NCBI_TaxID=1351;
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                                                                                                                                                                                                                                            Enterococcus faecalis Bacteria; Firmicutes;
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NCBI_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF260891; AAG23949.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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260891; AAG23949.1; -.
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25.0%;
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Bacillus/Clostridium grou
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Last annotation update)
(FRAGMENT).
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Pred. No. 7.
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les, from different strains
for production of ace during
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                                                                                                                                                                                                                                         group; Enterococcaceae;
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                                                                                     Murray B
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NON_TER
SEQUENCE
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01-MAR-2001 (TIEMBLIEL: 16,
01-MAR-2001 (TIEMBLIEL: 16,
01-MAR-2001 (TIEMBLIEL: 16,
                                                                                                                                                                                                                                                                                                           STRAIN-BE88/TX0860, HG6280/TX0630, HG10528/TX0631, AND HGMEDLINE-20407335; PubMed-10948146;
MAILLAPARRED S.R., Singh K.V., Duh R.W., Weinstock G.M.,
"Diversity of ace, a gene encoding a microbial surface or
recognizing adhesive matrix molecules, from different strengerococcus faecalis and evidence for production of ace
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis
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                                                                              TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS 170
                                                                                          TITSGNKSTNYTVHKSEAG---TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITSGNKSTNVTVHKSEAG---TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGEASGNQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATATQRLTIEGVTNTETGQIERDYPFFYKVGDLAGE-SNQVRWFLNVNLNKSDVTEDIS
QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                          IADROGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY 225
                                           IKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIP 134
                                                                                                                                                                                                                               t. Immun. 68:5210-5217(2000).
AF260892; AAG23950.1; -.
AF260884; AAG23942.1; -.
AF260885; AAG23943.1; -.
AF260886; AAG23944.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEGTVKGELKV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDKARFTSFIVRYTSTITEAGQHQATFKNSYDINYQLNNQDATNEKNTSQV-----KNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGYGSYNSFSINYKTKIT--NEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHNINANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IADRQGSGQQLNKESFTFDIVNDKETKY---ISLAEFEQQGYGKIDFV--TDNDFNLRFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t. Immun. 68:5210-5217(2000).
AF260887; AAG23945.1; -.
                                                                                                                                            Similarity
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296 AA;
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27.7%;
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27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                              Score 175; DB 2;
Pred. No. 1.1e-05;
4; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 175; DB 2
Pred. No. 1e-05;
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                                                                                                                                                                                                                                                                                                                                                 Murray B.E.;
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## ALIGNMENTS

Collagen binding protein M31 epitope DNA.

21-MAY-1998 (first entry)

AAT93437;

AAT93437 standard; DNA;

849 ВP سر

RESULT
AAT91437
ID AAT9
XX AAT9
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XX COL Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRANM; adhesin; vaccine; immunisation; diagnosis; therapy; epitope M31; ss. Hook M, WO9743314-A2 Staphylcoccus aureus. (UABR-) UAB RES FOUND. (TEXA ) UNIV TEXAS A & M SYSTEM. 16-MAY-1996; 14-MAY-1997; 20-NOV-1997. House-Pompeo K, Patti JM, 96US-0017678 97WO-US08210 Location/Qualifiers 253..849 Sthanam N, Symersky

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This nucleic acid comprises a portion of the Staphylococcus aureus cna gene that codes for collagen binding protein (CBP) epitope M31 (see AAW31553), i.e. amino acids 61-343 of full-length CBP. Claimed 441, 849 and 1500 bp nucleic acid sequences (see AAT93436-38) respectively encode CBP epitopes M17, M31 and M55 (see AAW31552-54)
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nes 849; Conserv
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DB; AAW31553.
                                               ACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAATT
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                               acattaaacattaatgtgacaggtacacatagcaattattatagtggacaaagtgcaatt
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cna gene that codes for collagen binding protein (CBP) epithope MS5 (see AAW31554), i.e. amino acids 30-531 of full-length CBP. Claimed 41, 849 and 1500 bp nucleic acid sequences (see AAW315436-38) respectively encode CBP epitopes M17, M31 and M55 (see AAW3152-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in
                                                                                                                                                                                                                                                                                                                                                                            Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                       This nucleic acid comprises a portion of the Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                             Claim 40;
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Best Local Similarity Matches 849; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGATAAAAATGGAAAAATACAAAATGGTGACATGATTAAAGTGGCCATGGCCGACAAGC
                                                                                                                                                                GAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGATTTAAGC
                       GATACCAAG 849
                                                           ACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATCAA
                                                                                                                                                                                                                                                                                                                                   ATTGATGTAACAATTCCACAAGGCTATGGGTCATATAAATAGTTTTTCAATTAACTACAAA 660
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                                                                                                        GCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAGGATAAA
                                                                                                                                           gagcatggtaaggaagtgaacgggaaatcatttaatcatactgtgcacaatattaat
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Pred. No. 1.1e-176;
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                                                                                                                                                                                                                                                                            1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 40pp; English.
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                                           atatgctaccaagaagatacgacacatgtacgatggtttttaaatattaacaatgaaaaa
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   GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG
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                                                                                                                                                                                                                             90SE-0003374
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This nucleic acid comprises a portion of the Staphylococcus aureus cna gene that codes for collagen binding protein (CBP) epitope M17 (see AAM31552), i.e. amino acids 151-297 of full-length CBP. Claime 441, 849 and 1500 bp nucleic acid sequences (see AAM3436-38) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen binding protein; cna gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                  Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
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epitope M17; ss.
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                                                                                                                                                                                                                                                                                                                                                Page 113; 143pp; English.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           screening, diagnostic and therapeutic applications including act and passive immunisation and methods for the prevention of bacterial colonisation in an animal such as a human. These DNA segments and the peptides encoded by them are also contemplated use in the preparation of vaccines and as carrier proteins in vaccine formulations, as well as in the formulation of composition the prevention of S. aureus infection.
                      26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                   01-FEB-2001
                                                                                                          WO200107665-A2
                                                                                                                                                      Electron-transfer group;
                                                                                                                                                                                            Oligonucleotide D1835
                                                                                                                                                                                                                                                                   AAF58252 standard;
                                                           26-JUL-2000;
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(CLIN-) CLINICAL MICRO SENSORS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGTTAATAATTCACAAGCT 711
                                                                                                                                                                                                                                                                                                                                                                                        TCATATAATAGTTTTTCAATTAACTACAAAACCAAAATTACGAATGAACAGCAAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATAACTGTTGATAATACGAAGAACACAATTGATGTAACAATTCCACAAGGCTATGGG
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                                                                                                                                                                                                                                                                                                                              tttgttaataattcacaagct 441
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                                                           2000WO-US20476
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                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                   936
                                                                                                                                                                  ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                   ВP
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Pred. No. 1.2e-87;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Umek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, us hybridization assays, e.g. for genotyping, allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monitoring
                                                                                                                                                                                                                                                                                  491
 131
                                                                                                                                                                                                                                                                                                                                                                                                                               671
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AAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTA 778
                                                                   AAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATC
                                                                                            CAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACA
                                                                                                                                       TTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACA
                                                                                                                                                                                      GCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGTGCAA
                                                                                                                                                                                                                                                          ATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGATTTAA
                                                                                                                                                                                                                                                                                  TGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAAAGTT
                                                                                                                                                                                                                                                                                                                                AAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGC
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                                                                                                                                                                                                                                     TTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAGATA
                                                                                                                                                                                                                                                                                                                                                                                AGGTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to a composition comprising two an electron-transfer group (ETM) having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 170; DB 22
Pred. No. 2.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 776 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 936;
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RESULT 6
AAF58254/c
ID AAF58254 standard; DNA;
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Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                   monitoring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-159728/16
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17-MAR-2000; 2000US-0190259.
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              AAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATG
                                                                              AAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGC
                                                                                                                                          AGGTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAG 178
                                                                                                                                                                                                         GCGGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAAC 118
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                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                      20.0%; Score 170; DB 22; Length 936; llarity 1.0%; Pred. No. 2.1e-28; Conservative 524; Mismatches 254; Indels
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17-MAR-2000;
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2000US-0190259
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                                                                                                          CAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACA
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                     ATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAGGATA
                                                                                                                                AAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATC
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2.1e-28;
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AC AAF582
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tive 524; Mismatches 254;
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                                                                    WPI; 2001-159728/16
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17-MAR-2000;
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                                                                                                                                    AAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTA 778
                                                                                                                                                                                                               AAAAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGC 238
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                                                        ANACCAAAATTACGAATGAACAGCAAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATC 718
                                                                                                                                                                                                                                       CAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAACTACA 658
                                                                                                                                                                                                                                                                    TTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAGAACA
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ilarity 1.0%; Pred. No. 2.1e-28;
Conservative 524; Mismatches 25
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 170; DB 22; ilarity 1.0%; Pred. No. 2.1e-28; Conservative 524; Mismatches 254;
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)

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surface Page 127;

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gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses of a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-159728/16
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17-MAR-2000; 2000US-0190259
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gene expression; ss.
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Best Local Similarity
Matches 4; Conserv
                      Oligonucleotide D2004
Electron-transfer group; ETM; mismatch; genotyping;
                                         24-APR-2001
                                                               AAF58259;
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 936 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                               19.1%; Score 162.4; ilarity 0.5%; Pred. No. 9.7e. Conservative 522; Mismatches
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AAF58262
                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
Sequence
                     monitoring gene expression.
                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses of a single surface.
                                                                                                                                                                        WPI; 2001-159728/16
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17-MAR-2000;
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gene expression; ss.
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                                                                                                   Example 6; Page 128; 159pp; English.
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139 C; 10 G;
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Query Match
Best Local Similarity
Matches 4; Conserv

19.1%; Score 162.4; DB ilarity 0.5%; Pred. No. 9.7e-27 Conservative 522; Mismatches 2:

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                                        723 GCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAATGC 782
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Search completed: January 29, 2002, 23:13:49 Job time: 3798 sec

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1: /cgn2_6/ptodata/2/
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Copyright (c) 1993 - 2000
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US-08-447-031A-8
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US-08-856-253-1
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US-08-856-253-1
US-08-868-826B-13
S231168-1
US-08-960-780-51
US-09-973-898-51
US-09-973-1913A-2
US-08-471-044-22
US-08-471-046-22
US-08-471-0464-19
US-08-471-0461-19
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	Sequence 8, Appli	Sequence 1137, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 186, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 41, Appl	Sequence 41, Appl	Sequence 595, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

## COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/856,253 FILING DATE: Concurrently Herewith CLASSIFICATION DATA: APPLICATION NATA: APPLICATION NUMBER: US 60/017,678 FILING DATE: 16-MAY-1996 ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara S. PRGISTRATION NUMBER: 33,928 PRGISTRATION NUMBER: TAMK:193 ; TOPOLOGY: linear US-08-856-253-3 US-08-856-253-3 REGISTRATION NUMBER: 33,928 REFERENCE/DOCKET NUMBER: TAMK TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEPAX: (512) 474-7577 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 849 base pairs TYPE: nucleic acid Sequence 3, Application Patent No. 6288214 GENERAL INFORMATION: APPLICANT: APPLICANT: Sthanam, Narayana APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 APPLICANT: STREET: P.O. BO CITY: Houston STATE: Texas COUNTRY: U.S. ZIP: 77210 STRANDEDNESS: Application US/08856253 Patti, Joseph M. House-Pompeo, Karen Hook, Magnus single

100.0%;

Score 849; DB 4; Pred. No. 4.5e-194;

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RESULT 2
US-08-856-253-5
                                                                                                                                                 Sequence 5, Application Patent No. 6288214 GENERAL INFORMATION:
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Patti, Joseph M.
House-Pompeo, Karen
Sthanam, Narayana
Symersky, Jindrich
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STRANDEDNESS:
TOPOLOGY: lin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 849; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COLLAGEN
TITLE OF INVENTION: AND METHO
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White &
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release (CURRENT APPLICATION NUMBER: US/08/8: APPLICATION NUMBER: US/08/8: FILING DATE: Concurrently HCCLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/0: APPLICATION NUMBER: APPLICATION NUM
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DC-DOSMS-DOS

OPERATING SYSTEM: DC-DOSMS-DOS

OPERATING SYSTEM: DC-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS-DOSMS
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,92
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STREET: P.O. BU
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
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CTACCAGAAGATACGACACTGTACGATGGTTTTTAAATATTAACAATGAAAAAAGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 849; DB 4; liarity 100.0%; Pred. No. 5.2e-194; Conservative 0; Mismatches 0;
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                                                      APPLICATION UNMER: US/08/447,031A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: PATTI, JOSEPH
APPLICANT: SIGNAS, Christer
APPLICANT: SWITALSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL
TITLE OF INVENTION: ITS PREPARATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   934
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                                                                                                                                                                                                                                                                            STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                   APPLICATION NUMBER: FILING DATE: 22-OC'
NAME: McGowan, Malc
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                       E: Burns, Doane, P.O. Box 1404
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JONSSON, Hans
LINDBERG, Martin
                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
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                                    MBER: SE 9003374-7
22-OCT-1990
Malcolm K.
MBER: 39,300
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SEQUENCE CHARACTERISTICS:
LENGTH: 3827 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HOLECTLE TYPE: DNA (genomic
US-08-447-031A-1
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Best Local Similarity
Matches 849; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
1111
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                                                GAGCATGGTAAGGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAATATTAAT
                                                                                                               ACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGGTATCAA 720
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US-08-447-031A-8
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US-08-447-031A-8
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                   Query Match
Best Local Similarity
Matches 836; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION UMBER: US/08/447,031A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
APPLICATION TONCAUTON.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
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1171 GATACCAAG 1179
NAME: MCGOWAN, MAICOLM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) FEATURE:
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TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS
TITLE OF INVENTION: ITS PREPARATION
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STATE: Virginia
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HOOK, Magnus
JONSSON, Hans
LINDBERG, Martin
PATTI, Joseph
SIGNAS, Christer
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Conservative
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                                                                     Score 792.2; DB 2;
Pred. No. 2.4e-180;
0; Mismatches 13;
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O8-856-253-1 08-856-253-1 equence 1, Application US/08856253 atent No. 6288214 GENERAL INFORMATION: APPLICANT: Hook, Magnus APPLICANT: Patti, Joseph M. APPLICANT: Sthanam, Narayana APPLICANT: Symersky, Jindrich TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee	GATAAAGATACCAAG 849 	ATTAATGCTAATGCCGGTATTGAAGGTACTGTAAAAGGTGAATTAAAAGTTTTAAAACAG 834 	TATCAAGAGCATGGTAAGGAAGAAGTGAACGGGAAATCATTTAATCATACTGTGCACAAT 774	TACAAAACCAAAATTACGAATGAACAGCAAAAAGAGTTTGTTAATAATTCACAAGCTTGG 714	AACACAATTGATGTAACAATTCCACAAGGCTATGGGTCATATAATAGTTTTTCAATTAAC 654	GCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAATAACTGTTGATAATACGAAG 594 	TTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGACAAAGT 534 	AGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTGGACAGCAGTTAGAT 474	ATATGCTACC-AGAAGATACGACACATGTACGATGGTTTTTAAATATTAACAATGAAAAA 414 	ACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCTATTATAAAACGGGAG 355	ACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTGGGAATAAATCAACGAATGTT 300 	AAATTAAGTGATGTTTCGGGATTTGCAGAATTTGAAGTACAAGGAAGAAATTTAACGCAA 240 	GTGGGTCAAGCAGTTATTACACCAGACGGTGCAACAATTACATTCAATGATAAAGTAGAA 180 	GGTACAGTAAAGATAGAGGGTTATAGTAAAACAGTACCATTAACTGTTAAAGGTGAACAG 120 

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RESULT 6
US-08-332-463-14/c
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: CONCULTENT)
CLASSIFICATION: 514
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LENGTH: 441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 66
-FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
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COUNTRY: U.L.
77210
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                      TTTGTTAATAATTCACAAGCT 441
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(512) 474-757
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Best Local Similarity
Matches 27; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: v..
STATE: v..
COUNTRY: USA
COUNTRY: 22313-029
TD: 270ADABLE F
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                               101 TAACTGTTAAAGGTGAACAGGTGGGTCAAGCAGTTATTACACCAGACGAGCGGTGCAACAATTA 160
                                                                                                                                                                                                                              221 AAGGAAGAATTTAACGCAAACAAATACTTCAGATGACAAAGTAGCTACGATAACATCTG
401 TTAACAATGAAAAAAGTTATGTATCGAAAGATATTACTATAAAGGATCAGATTCAAGGTG 460
                                                                                                                                                       281 GGAATAAATCAACGAATGTTACGGTTCATAAAAGTGAAGCGGGAACAAGTAGTGTTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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TELEFAX: (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: pTzgpt-F1s
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                                                                            ATTATAAAACGGGAGATATGCTACCAGAAGATACGACACATGTACGATGGTTTTTAAATA 400
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                                      7218 base pairs
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1800 Diagonal Road, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 64.2; DB 1; Length 7 ilarity 6.5%; Pred. No. 1.1e-06; Conservative 225; Mismatches 163; Indels
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26-AUG-1991
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Sequence 13, App...
                                                                                                                                                                        Matches
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                     -08-487-826B-13
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                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: :
                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                      354 AGATATGCTACCAGAAGATACGACATGTACGATGGTTTTTAAATATTTAACAATGAAAA 413
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530 AAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAAATAACTGTTGATAATA 589
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CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: NIH121.001CP1
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                       TTT----AAGCACATTAAACATTAATGTGACAGGTACACATAGCAATTATTATAGTGGAC 529
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Wellems,
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Chitnis, Chetan
Miller, Louis H.
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Su, Xin-zhaun
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RESULT 8
5231168-1
; Patent No. 5231168
; PATENT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN,
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PAI
TITLE OF INVENTION MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATE
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Best Local Similarity 42.4%;
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                                                             aatagtagaggttgaagaaattctaccagaagataaaaatgaaaaagttcaacatgaaat 1784
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TTATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGCCTTTCCAGGTTCTAAAAT 575
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                                                                                                                                 AGGTGGACAGCTTAGATTTAAGCACATTAAACATTAATGTGACAGGTACACATAGCAA 515
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US-08-960-780-51; Sequence 51, App; Patent No. 62044
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                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                            NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                           APPLICATION NUMBER: US 60/029,848 FILING DATE: 30-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: U5/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PARIOR PAPLICATION DATA:
PARIOR CAPPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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   MOLECULE TYPE:
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                  TOPOLOGY:
                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                               LENGTH:
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DNA (genomic)
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               ATTORNEY/AGENT INFORMATION:
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US-09-073-898-51
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Best Local Similarity
Matches 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
                 APPLICATION NUMBER:
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
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   FILING DATE:
                                                                                                               CLASSIFICATION:
                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                         STATE:
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                     Morrill, George
Finstad-Lee, Stacey
VENTION: No. 6242669el Pesticidal Toxins and Nucleotide
VENTION: Sequences Which Encode These Toxins
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Narva, Kenneth E.
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JMBER: US 08/960,780
30-OCT-1997
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                                                                                                                                                                                        Version #1.30
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                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1341
TYPE: DNA
ORGANISM: Bacillus laterosporus
Query Match
Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Strains
TITLE OF INVENTION: Strains
TITLE OF INVENTION: WINDER: Uf
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Patent No. 6297369
                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/1
PRIOR EILING DATE: 1999-0-6
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/371,913A
CURRENT FILING DATE: 199-08-10
PRIOR APPLICATION NUMBER: 60/095,955
PRIOR FILING DATE: 1998-08-10
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
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STRANDEDNESS: single
TOPOLOGY: linear
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Stockhoff, Brian A.
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Score 42.8; DB 4;
Pred. No. 0.091;
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                  INFORMATION FOR SEQ ID NO:
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                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8582
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIO
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 FILING DATE: 09-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
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                                                                                                   NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                FILING DATE:
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                                 919-541-8689
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Koziel, Michael G
Mullins, Martha A
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Kostichka, N. Kristy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                       UMBER: US 08/037,057
25-MAR-1993
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                                                                                                                                                                                                                                                                                      US 08/314,594
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NAME/KEY: CDS
LOCATION: 1..4038
OTHER INFORMATION:
CTHER INFORMATION:
US-08-471-033-22
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US-08-471-044-22
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Patent No. 5840868
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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                                                             APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995 CLASSIFICATION: 800
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                                                                                                                                                                                                                                                    COUNTRY:
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CITY: Hawthorne
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Kostichka, N. Kristy
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Koziel, Michael G
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product"
                                                                                                    US/08/471,044
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                                                                                                                                         Version #1.30B
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                                                                                                                                                                                                                              Sequence 22, Patent No. 5
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
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LENGTH: 4041 base pair
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APPLICATION NUMBER:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: linear
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REGISTRATION NUMBER: 40,403
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                                                          Kostichka, N. Kristy
Duck, Nicholas B
                                                                                            Desai, Nalini M
                                                                                                              Carr, Brian
                                                                                                                                                 Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
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                                                                                                                               Nye, Gordon J
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Pred. No. 0.12;
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Best Local Similarity 47.4%;
Matches 128; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEPAX: 919-541-8689
FORMATION FOR CEP TELEPAX: 1919-541-8689
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,483A
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/314,594
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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NAME: Spruill, W. Murrav
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                                                                                                                   633 ATATAATAGTTTTTCAATTAACTACAAAAC 662
                                                                                                                                                        489 TACGATTAATTCTGATGCAATGGCACAGTTTAAAGAACAATTTTTAGATAGGGATATTAA 548
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                          CAATTATTATAGTGGACAAAGTGCAATTACTGATTTTGAAAAAGGCCTTTCCCAGGTTCTAA 572
                                                                                                                                                                                                                                     CACCTATAAAAATGTGGAACCGACAACAATTGGATTTAATAAATCTTTAACAGAAGGTAA
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                                                                   Matches
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,046A
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4041 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Method For Iso
TITLE OF INVENTION: Protein Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
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APPLICATION NUMBER: US 08/463,483
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                   393 TITAAATATTAACAATGAAAAAAGTTATGTATGGAAAGATATTACTATAAAGGATCAGAT 452
309 TATAAAGACAAATTATAAAGAAATTACTTTTTCTATGGCAGGCTCATTTGAAGATGAAAT 368
                                                                                                                                                                      LOCATION: 1..4038
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: CG
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Kostichka, N. Kristy
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Koziel, Michael
                                                                   Conservative
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product"
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                                                                 Score 42.8; DB 2;
Pred. No. 0.12;
0; Mismatches 142.
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